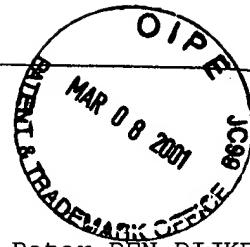


SEQUENCE LISTING



\ (1) GENERAL INFORMATION:

(i) APPLICANT: Kohei MIYAZONO; Takeshe IMAMURA; Peter DEN DIJKE

(ii) TITLE OF INVENTION: ISOLATED ALK-1 PROTEIN, NUCLEIC ACIDS ENCODING IT, AND USES THEREOF

(iii) NUMBER OF SEQUENCES: 46

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Fulbright & Jaworski L.L.P.
(B) STREET: 666 Fifth Avenue
(C) CITY: New York City
(D) STATE: New York
(E) COUNTRY: USA
(F) ZIP: 10103

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette, 3.25 inch, 1.44mb
(B) COMPUTER: IBM PS/2
(C) OPERATING SYSTEM: PC-DOS
(D) SOFTWARE: Wordperfect

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 09/267,963
(B) FILING DATE: March 12, 1999
(C) CLASSIFICATION: 435

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: PCT/GB93/02367
(B) FILING DATE: November 17, 1993

*C
Cont*

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: GB 9224057.1
(B) FILING DATE: November 17, 1992

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: GB 9304677.9
(B) FILING DATE: March 8, 1993

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: GB 9304680.3
(B) FILING DATE: March 8, 1993

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 9311047.6
(B) FILING DATE: May 28, 1993

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 9313763.6
(B) FILING DATE: July 2, 1993

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 9136099.2
(B) FILING DATE: August 3, 1993

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 321344.5
(B) FILING DATE: October 15, 1993

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 09/039,177
(B) FILING DATE: March 13, 1998

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Mary Anne Schofield
(B) REGISTRATION NUMBER: 36,669
(C) REFERENCE/DOCKET NUMBER: LUD 5539.1 CIP - JEL/MAS

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (212) 318-3000
(B) TELEFAX: (212) 318-3400

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1984 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 283..1791

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

AGGAAACGGT TTATTAGGAG GGAGTGGTGG AGCTGGCCA GGCAGGAAGA CGCTGGAATA 60

AGAAACATTT TTGCTCCAGC CCCCATCCCA GTCCCGGGAG GCTGCCGCGC CAGCTGCGCC 120

GAGCGAGCCC CTCCCCGGCT CCAGCCCGGT CCGGGGCCGC GCCGGACCCC AGCCCGCCGT 180

CCAGCGCTGG CGGTGCAACT GCGGCCGCGC GGTGGAGGGG AGGTGGCCCC GGTCCGCCGA 240

AGGCTAGCGC CCCGCCACCC GCAGAGCGGG CCCAGAGGGA CC ATG ACC TTG GGC Met Thr Leu Gly	294
1	
TCC CCC AGG AAA GGC CTT CTG ATG CTG ATG GCC TTG GTG ACC CAG Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala Leu Val Thr Gln	342
5 10 15 20	
GGA GAC CCT GTG AAG CCG TCT CGG GGC CCG CTG GTG ACC TGC ACG TGT Gly Asp Pro Val Lys Pro Ser Arg Gly Pro Leu Val Thr Cys Thr Cys	390
25 30 35	
GAG AGC CCA CAT TGC AAG GGG CCT ACC TGC CGG GGG GCC TGG TGC ACA Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly Ala Trp Cys Thr	438
40 45 50	
GTA GTG CTG GTG CGG GAG GGG AGG CAC CCC CAG GAA CAT CGG GGC Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln Glu His Arg Gly	486
55 60 65	
TGC GGG AAC TTG CAC AGG GAG CTC TGC AGG GGG CGC CCC ACC GAG TTC Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg Pro Thr Glu Phe	534
70 75 80	
GTC AAC CAC TAC TGC TGC GAC AGC CAC CTC TGC AAC CAC AAC GTG TCC Val Asn His Tyr Cys Cys Asp Ser His Leu Cys Asn His Asn Val Ser	582
85 90 95 100	
CTG GTG CTG GAG GCC ACC CAA CCT CCT TCG GAG CAG CCG GGA ACA GAT Leu Val Leu Glu Ala Thr Gln Pro Pro Ser Glu Gln Pro Gly Thr Asp	630
105 110 115	
GGC CAG CTG GCC CTG ATC CTG GGC CCC GTG CTG GCC TTG CTG GCC CTG Gly Gln Leu Ala Leu Ile Leu Gly Pro Val Leu Ala Leu Leu Ala Leu	678
120 125 130	
GTG GCC CTG GGT GTC CTG GGC CTG TGG CAT GTC CGA CGG AGG CAG GAG Val Ala Leu Gly Val Leu Gly Leu Trp His Val Arg Arg Arg Gln Glu	726
135 140 145	
AAG CAG CGT GGC CTG CAC AGC GAG CTG GGA GAG TCC AGT CTC ATC CTG Lys Gln Arg Gly Leu His Ser Glu Leu Gly Glu Ser Ser Leu Ile Leu	774
150 155 160	
AAA GCA TCT GAG CAG GGC GAC ACG ATG TTG GGG GAC CTC CTG GAC AGT Lys Ala Ser Glu Gln Gly Asp Thr Met Leu Gly Asp Leu Leu Asp Ser	822
165 170 175 180	
GAC TGC ACC ACA GGG AGT GGC TCA GGG CTC CCC TTC CTG GTG CAG AGG Asp Cys Thr Thr Gly Ser Gly Ser Gly Leu Pro Phe Leu Val Gln Arg	870
185 190 195	
ACA GTG GCA CGG CAG GTT GCC TTG GTG GAG TGT GTG GGA AAA GGC CGC Thr Val Ala Arg Gln Val Ala Leu Val Glu Cys Val Gly Lys Gly Arg	918
200 205 210	

TAT GGC GAA GTG TGG CGG GGC TTG TGG CAC GGT GAG AGT GTG GCC GTC Tyr Gly Glu Val Trp Arg Gly Leu Trp His Gly Glu Ser Val Ala Val 215 220 225	966
AAG ATC TTC TCC TCG AGG GAT GAA CAG TCC TGG TTC CGG GAG ACT GAG Lys Ile Phe Ser Ser Arg Asp Glu Gln Ser Trp Phe Arg Glu Thr Glu 230 235 240	1014
ATC TAT AAC ACA GTA TTG CTC AGA CAC GAC AAC ATC CTA GGC TTC ATC Ile Tyr Asn Thr Val Leu Leu Arg His Asp Asn Ile Leu Gly Phe Ile 245 250 255 260	1062
GCC TCA GAC ATG ACC TCC CGC AAC TCG ACG CAG CTG TGG CTC ATC Ala Ser Asp Met Thr Ser Arg Asn Ser Ser Thr Gln Leu Trp Leu Ile 265 270 275	1110
ACG CAC TAC CAC GAG CAC GGC TCC CTC TAC GAC TTT CTG CAG AGA CAG Thr His Tyr His Glu His Gly Ser Leu Tyr Asp Phe Leu Gln Arg Gln 280 285 290	1158
ACG CTG GAG CCC CAT CTG GCT CTG AGG CTA GCT GTG TCC GCG GCA TGC Thr Leu Glu Pro His Leu Ala Leu Arg Leu Ala Val Ser Ala Ala Cys 295 300 305	1206
GGC CTG GCG CAC CTG CAC GTG GAG ATC TTC GGT ACA CAG GGC AAA CCA Gly Leu Ala His Leu His Val Glu Ile Phe Gly Thr Gln Gly Lys Pro 310 315 320	1254
GCC ATT GCC CAC CGC GAC TTC AAG AGC CGC AAT GTG CTG GTC AAG AGC Ala Ile Ala His Arg Asp Phe Lys Ser Arg Asn Val Leu Val Lys Ser 325 330 335 340	1302
AAC CTG CAG TGT TGC ATC GCC GAC CTG GGC CTG GCT GTG ATG CAC TCA Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly Leu Ala Val Met His Ser 345 350 355	1350
CAG GGC AGC GAT TAC CTG GAC ATC GGC AAC AAC CCG AGA GTG GGC ACC Gln Gly Ser Asp Tyr Leu Asp Ile Gly Asn Asn Pro Arg Val Gly Thr 360 365 370	1398
AAG CGG TAC ATG GCA CCC GAG GTG CTG GAC GAG CAG ATC CGC ACG GAC Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Gln Ile Arg Thr Asp 375 380 385	1446
TGC TTT GAG TCC TAC AAG TGG ACT GAC ATC TGG GCC TTT GGC CTG GTG Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala Phe Gly Leu Val 390 395 400	1494
CTG TGG GAG ATT GCC CGC CGG ACC ATC GTG AAT GGC ATC GTG GAG GAC Leu Trp Glu Ile Ala Arg Arg Thr Ile Val Asn Gly Ile Val Glu Asp 405 410 415 420	1542

TAT AGA CCA CCC TTC TAT GAT GTG GTG CCC AAT GAC CCC AGC TTT GAG Tyr Arg Pro Pro Phe Tyr Asp Val Val Pro Asn Asp Pro Ser Phe Glu 425 430 435	1590
GAC ATG AAG AAG GTG GTG TGT GTG GAT CAG CAG ACC CCC ACC ATC CCT Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr Pro Thr Ile Pro 440 445 450	1638
AAC CGG CTG GCT GCA GAC CCG GTC CTC TCA GGC CTA GCT CAG ATG ATG Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu Ala Gln Met Met 455 460 465	1686
CGG GAG TGC TGG TAC CCA AAC CCC TCT GCC CGA CTC ACC GCG CTG CGG Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu Thr Ala Leu Arg 470 475 480	1734
ATC AAG AAG ACA CTA CAA AAA ATT AGC AAC AGT CCA GAG AAG CCT AAA Ile Lys Lys Thr Leu Gln Lys Ile Ser Asn Ser Pro Glu Lys Pro Lys 485 490 495 500	1782
G TG ATT CAA TAGCCCAGGA GCACCTGATT CCTTTCTGCC TGCAGGGGGC Val Ile Gln	1831
TGGGGGGGTG GGGGGCAGTG GATGGTGCCC TATCTGGTA GAGGTAGTGT GAGTGTGGTG	1891
TGTGCTGGGG ATGGGCAGCT GCGCCTGCCT GCTCGGCC CAGCCCACCC AGCCAAAAAT	1951
ACAGCTGGGC TGAAACCTGA AAAAAAAA AAA	1984

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 503 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Thr Leu Gly Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala			
1 5 10 15			
Leu Val Thr Gln Gly Asp Pro Val Lys Pro Ser Arg Gly Pro Leu Val			
20 25 30			
Thr Cys Thr Cys Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly			
35 40 45			
Ala Trp Cys Thr Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln			
50 55 60			
Glu His Arg Gly Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg			
65 70 75 80			
Pro Thr Glu Phe Val Asn His Tyr Cys Cys Asp Ser His Leu Cys Asn			
85 90 95			
His Asn Val Ser Leu Val Leu Glu Ala Thr Gln Pro Pro Ser Glu Gln			
100 105 110			

Pro Gly Thr Asp Gly Gln Leu Ala Leu Ile Leu Gly Pro Val Leu Ala
115 120 125
Leu Leu Ala Leu Val Ala Leu Gly Val Leu Gly Leu Trp His Val Arg
130 135 140

Arg Arg Gln Glu Lys Gln Arg Gly Leu His Ser Glu Leu Gly Glu Ser
145 150 155 160
Ser Leu Ile Leu Lys Ala Ser Glu Gln Gly Asp Thr Met Leu Gly Asp
165 170 175
Leu Leu Asp Ser Asp Cys Thr Thr Gly Ser Gly Ser Gly Leu Pro Phe
180 185 190
Leu Val Gln Arg Thr Val Ala Arg Gln Val Ala Leu Val Glu Cys Val
195 200 205
Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg Gly Leu Trp His Gly Glu
210 215 220
Ser Val Ala Val Lys Ile Phe Ser Ser Arg Asp Glu Gln Ser Trp Phe
225 230 235 240
Arg Glu Thr Glu Ile Tyr Asn Thr Val Leu Leu Arg His Asp Asn Ile
245 250 255
Leu Gly Phe Ile Ala Ser Asp Met Thr Ser Arg Asn Ser Ser Thr Gln
260 265 270
Leu Trp Leu Ile Thr His Tyr His Glu His Gly Ser Leu Tyr Asp Phe
275 280 285
Leu Gln Arg Gln Thr Leu Glu Pro His Leu Ala Leu Arg Leu Ala Val
290 295 300
Ser Ala Ala Cys Gly Leu Ala His Leu His Val Glu Ile Phe Gly Thr
305 310 315 320
Gln Gly Lys Pro Ala Ile Ala His Arg Asp Phe Lys Ser Arg Asn Val
325 330 335
Leu Val Lys Ser Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly Leu Ala
340 345 350
Val Met His Ser Gln Gly Ser Asp Tyr Leu Asp Ile Gly Asn Asn Pro
355 360 365
Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Gln
370 375 380
Ile Arg Thr Asp Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala
385 390 395 400
Phe Gly Leu Val Leu Trp Glu Ile Ala Arg Arg Thr Ile Val Asn Gly
405 410 415
Ile Val Glu Asp Tyr Arg Pro Pro Phe Tyr Asp Val Val Pro Asn Asp
420 425 430
Pro Ser Phe Glu Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr
435 440 445
Pro Thr Ile Pro Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu
450 455 460
Ala Gln Met Met Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu
465 470 475 480
Thr Ala Leu Arg Ile Lys Lys Thr Leu Gln Lys Ile Ser Asn Ser Pro
485 490 495
Glu Lys Pro Lys Val Ile Gln
500

(2) INFORMATION FOR SEQ ID NO: 3:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2724 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 104..1630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CTCCGAGTAC CCCAGTGACC AGAGTGAGAG AAGCTCTGAA CGAGGGCACG CGGCTTGAAG	60
GA CTGTGGGC AGATGTGACC AAGAGCCTGC ATTAAGTTGT ACA ATG GTA GAT GGA	115
Met Val Asp Gly	
1	
GTG ATG ATT CTT CCT GTG CTT ATC ATG ATT GCT CTC CCC TCC CCT AGT	163
Val Met Ile Leu Pro Val Leu Ile Met Ile Ala Leu Pro Ser Pro Ser	
5 10 15 20	
ATG GAA GAT GAG AAG CCC AAG GTC AAC CCC AAA CTC TAC ATG TGT GTG	211
Met Glu Asp Glu Lys Pro Lys Val Asn Pro Lys Leu Tyr Met Cys Val	
25 30 35	
TGT GAA GGT CTC TCC TGC GGT AAT GAG GAC CAC TGT GAA GGC CAG CAG	259
Cys Glu Gly Leu Ser Cys Gly Asn Glu Asp His Cys Glu Gly Gln Gln	
40 45 50	
TGC TTT TCC TCA CTG AGC ATC AAC GAT GGC TTC CAC GTC TAC CAG AAA	307
Cys Phe Ser Ser Leu Ser Ile Asn Asp Gly Phe His Val Tyr Gln Lys	
55 60 65	
GGC TGC TTC CAG GTT TAT GAG CAG GGA AAG ATG ACC TGT AAG ACC CCG	355
Gly Cys Phe Gln Val Tyr Glu Gln Gly Lys Met Thr Cys Lys Thr Pro	
70 75 80	
CCG TCC CCT GGC CAA GCT GTG GAG TGC TGC CAA GGG GAC TGG TGT AAC	403
Pro Ser Pro Gly Gln Ala Val Glu Cys Cys Gln Gly Asp Trp Cys Asn	
85 90 95 100	

AGG AAC ATC ACG GCC CAG CTG CCC ACT AAA GGA AAA TCC TTC CCT GGA Arg Asn Ile Thr Ala Gln Leu Pro Thr Lys Gly Lys Ser Phe Pro Gly 105 110 115	451
ACA CAG AAT TTC CAC TTG GAG GTT GGC CTC ATT ATT CTC TCT GTA GTG Thr Gln Asn Phe His Leu Glu Val Gly Leu Ile Ile Leu Ser Val Val 120 125 130	499
TTC GCA GTA TGT CTT TTA GCC TGC CTG CTG GGA GTT GCT CTC CGA AAA Phe Ala Val Cys Leu Leu Ala Cys Leu Leu Gly Val Ala Leu Arg Lys 135 140 145	547
TTT AAA AGG CGC AAC CAA GAA CGC CTC AAT CCC CGA GAC GTG GAG TAT Phe Lys Arg Arg Asn Gln Glu Arg Leu Asn Pro Arg Asp Val Glu Tyr 150 155 160	595
GGC ACT ATC GAA GGG CTC ATC ACC ACC AAT GTT GGA GAC AGC ACT TTA Gly Thr Ile Glu Gly Leu Ile Thr Thr Asn Val Gly Asp Ser Thr Leu 165 170 175 180	643
GCA GAT TTA TTG GAT CAT TCG TGT ACA TCA GGA AGT GGC TCT GGT CTT Ala Asp Leu Leu Asp His Ser Cys Thr Ser Gly Ser Gly Ser Gly Leu 185 190 195	691
CCT TTT CTG GTA CAA AGA ACA GTG GCT CGC CAG ATT ACA CTG TTG GAG Pro Phe Leu Val Gln Arg Thr Val Ala Arg Gln Ile Thr Leu Leu Glu 200 205 210	739
TGT GTC GGG AAA GGC AGG TAT GGT GAG GTG TGG AGG GGC AGC TGG CAA Cys Val Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg Gly Ser Trp Gln 215 220 225	787
GGG GAA AAT GTT GCC GTG AAG ATC TTC TCC TCC CGT GAT GAG AAG TCA Gly Glu Asn Val Ala Val Lys Ile Phe Ser Ser Arg Asp Glu Lys Ser 230 235 240	835
TGG TTC AGG GAA ACG GAA TTG TAC AAC ACT GTG ATG CTG AGG CAT GAA Trp Phe Arg Glu Thr Glu Leu Tyr Asn Thr Val Met Leu Arg His Glu 245 250 255 260	883
AAT ATC TTA GGT TTC ATT GCT TCA GAC ATG ACA TCA AGA CAC TCC AGT Asn Ile Leu Gly Phe Ile Ala Ser Asp Met Thr Ser Arg His Ser Ser 265 270 275	931
ACC CAG CTG TGG TTA ATT ACA CAT TAT CAT GAA ATG GGA TCG TTG TAC Thr Gln Leu Trp Leu Ile Thr His Tyr His Glu Met Gly Ser Leu Tyr 280 285 290	979
GAC TAT CTT CAG CTT ACT ACT CTG GAT ACA GTT AGC TGC CTT CGA ATA Asp Tyr Leu Gln Leu Thr Thr Leu Asp Thr Val Ser Cys Leu Arg Ile 295 300 305	1027

GTG CTG TCC ATA GCT AGT GGT CTT GCA CAT TTG CAC ATA GAG ATA TTT Val Leu Ser Ile Ala Ser Gly Leu Ala His Leu His Ile Glu Ile Phe 310 315 320	1075
GGG ACC CAA GGG AAA CCA GCC ATT GCC CAT CGA GAT TTA AAG AGC AAA Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Lys 325 330 335 340	1123
AAT ATT CTG GTT AAG AAG AAT GGA CAG TGT TGC ATA GCA GAT TTG GGC Asn Ile Leu Val Lys Lys Asn Gly Gln Cys Cys Ile Ala Asp Leu Gly 345 350 355	1171
CTG GCA GTC ATG CAT TCC CAG AGC ACC AAT CAG CTT GAT GTG GGG AAC Leu Ala Val Met His Ser Gln Ser Thr Asn Gln Leu Asp Val Gly Asn 360 365 370	1219
AAT CCC CGT GTG GGC ACC AAG CGC TAC ATG GCC CCC GAA GTT CTA GAT Asn Pro Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp 375 380 385	1267
GAA ACC ATC CAG GTG GAT TGT TTC GAT TCT TAT AAA AGG GTC GAT ATT Glu Thr Ile Gln Val Asp Cys Phe Asp Ser Tyr Lys Arg Val Asp Ile 390 395 400	1315
TGG GCC TTT GGA CTT GTT TTG TGG GAA GTG GCC AGG CGG ATG GTG AGC Trp Ala Phe Gly Leu Val Leu Trp Glu Val Ala Arg Arg Met Val Ser 405 410 415 420	1363
AAT GGT ATA GTG GAG GAT TAC AAG CCA CCG TTC TAC GAT GTG GTT CCC Asn Gly Ile Val Glu Asp Tyr Lys Pro Pro Phe Tyr Asp Val Val Pro 425 430 435	1411
AAT GAC CCA AGT TTT GAA GAT ATG AGG AAG GTA GTC TGT GTG GAT CAA Asn Asp Pro Ser Phe Glu Asp Met Arg Lys Val Val Cys Val Asp Gln 440 445 450	1459
CAA AGG CCA AAC ATA CCC AAC AGA TGG TTC TCA GAC CCG ACA TTA ACC Gln Arg Pro Asn Ile Pro Asn Arg Trp Phe Ser Asp Pro Thr Leu Thr 455 460 465	1507
TCT CTG GCC AAG CTA ATG AAA GAA TGC TGG TAT CAA AAT CCA TCC GCA Ser Leu Ala Lys Leu Met Lys Glu Cys Trp Tyr Gln Asn Pro Ser Ala 470 475 480	1555
AGA CTC ACA GCA CTG CGT ATC AAA AAG ACT TTG ACC AAA ATT GAT AAT Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Thr Lys Ile Asp Asn 485 490 495 500	1603
TCC CTC GAC AAA TTG AAA ACT GAC TGT TGACATTTTC ATAGTGTCAA Ser Leu Asp Lys Leu Lys Thr Asp Cys 505	1650
GAAGGAAGAT TTGACGTTGT TGTCATTGTC CAGCTGGGAC CTAATGCTGG CCTGACTGGT	1710

TGTCAGAATG	GAATCCATCT	GTCTCCCTCC	CCAAATGGCT	GCTTGACAA	GGCAGACGTC	1770
GTACCCAGCC	ATGTGTTGGG	GAGACATCAA	AACCACCCCTA	ACCTCGCTCG	ATGACTGTGA	1830
ACTGGGCATT	TCACGAACTG	TTCACACTGC	AGAGACTAAT	GTTGGACAGA	CACTGTTGCA	1890
AAGGTAGGGA	CTGGAGGAAC	ACAGAGAAAT	CCTAAAAGAG	ATCTGGGCAT	TAAGTCAGTG	1950
GCTTTGCATA	GCTTCACAA	GTCTCCTAGA	CACTCCCCAC	GGGAAACTCA	AGGAGGTGGT	2010
GAATTTTAA	TCAGCAATAT	TGCCTGTGCT	TCTCTTCTTT	ATTGCACTAG	GAATTCTTG	2070
CATTCCCTTAC	TTGCACTGTT	ACTCTTAATT	TTAAAGACCC	AACTGCCAA	AATGTTGGCT	2130
GCGTACTCCA	CTGGTCTGTC	TTGGATAAT	AGGAATTCAA	TTGGCAAAA	CAAAATGTAA	2190
TGTCAGACTT	TGCTGCATT	TACACATGTG	CTGATGTTA	CAATGATGCC	GAACATTAGG	2250
AATTGTTTAT	ACACAACCTT	GCAAATTATT	TATTACTTGT	GCACCTAGTA	GTTTTACAA	2310
AACTGCTTTG	TGCATATGTT	AAAGCTTATT	TTTATGTGGT	CTTATGATTT	TATTACAGAA	2370
ATGTTTTAA	CACTATACTC	AAAATGGAC	ATTTCTTTT	ATTATCAGTT	AAAATCACAT	2430
TTTAAGTGCT	TCACATTTGT	ATGTGTTAG	ACTGTAACCT	TTTTCAGTT	CATATGCAGA	2490
ACGTATTTAG	CCATTACCCA	CGTGACACCA	CCGAATATAT	TATCGATTAA	GAAGCAAAGA	2550
TTTCAGTAGA	ATTTTAGTCC	TGAACGCTAC	GGGGAAAATG	CATTTCTTC	AGAATTATCC	2610
ATTACGTGCA	TTTAAACTCT	GCCAGAAAAA	AATAACTATT	TTGTTTTAAT	CTACTTTTG	2670
TATTTAGTAG	TTATTTGTAT	AAATTAATAA	AACTGTTTTC	AAGTCAAAAAA	AAAA	2724

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met	Val	Asp	Gly	Val	Met	Ile	Leu	Pro	Val	Leu	Ile	Met	Ile	Ala	Leu
1					5				10					15	
Pro	Ser	Pro	Ser	Met	Glu	Asp	Glu	Lys	Pro	Lys	Val	Asn	Pro	Lys	Leu
					20				25					30	
Tyr	Met	Cys	Val	Cys	Glu	Gly	Leu	Ser	Cys	Gly	Asn	Glu	Asp	His	Cys
					35			40				45			
Glu	Gly	Gln	Gln	Cys	Phe	Ser	Ser	Leu	Ser	Ile	Asn	Asp	Gly	Phe	His
					50			55				60			

Val Tyr Gln Lys Gly Cys Phe Gln Val Tyr Glu Gln Gly Lys Met Thr
65 70 75 80
Cys Lys Thr Pro Pro Ser Pro Gly Gln Ala Val Glu Cys Cys Gln Gly
85 90 95
Asp Trp Cys Asn Arg Asn Ile Thr Ala Gln Leu Pro Thr Lys Gly Lys
100 105 110
Ser Phe Pro Gly Thr Gln Asn Phe His Leu Glu Val Gly Leu Ile Ile
115 120 125
Leu Ser Val Val Phe Ala Val Cys Leu Leu Ala Cys Leu Leu Gly Val
130 135 140
Ala Leu Arg Lys Phe Lys Arg Arg Asn Gln Glu Arg Leu Asn Pro Arg
145 150 155 160
Asp Val Glu Tyr Gly Thr Ile Glu Gly Leu Ile Thr Thr Asn Val Gly
165 170 175
Asp Ser Thr Leu Ala Asp Leu Leu Asp His Ser Cys Thr Ser Gly Ser
180 185 190
Gly Ser Gly Leu Pro Phe Leu Val Gln Arg Thr Val Ala Arg Gln Ile
195 200 205
Thr Leu Leu Glu Cys Val Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg
210 215 220
Gly Ser Trp Gln Gly Glu Asn Val Ala Val Lys Ile Phe Ser Ser Arg
225 230 235 240
Asp Glu Lys Ser Trp Phe Arg Glu Thr Glu Leu Tyr Asn Thr Val Met
245 250 255
Leu Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ser Asp Met Thr Ser
260 265 270
Arg His Ser Ser Thr Gln Leu Trp Leu Ile Thr His Tyr His Glu Met
275 280 285
Gly Ser Leu Tyr Asp Tyr Leu Gln Leu Thr Thr Leu Asp Thr Val Ser
290 295 300
Cys Leu Arg Ile Val Leu Ser Ile Ala Ser Gly Leu Ala His Leu His
305 310 315 320
Ile Glu Ile Phe Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp
325 330 335
Leu Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Gln Cys Cys Ile
340 345 350
Ala Asp Leu Gly Leu Ala Val Met His Ser Gln Ser Thr Asn Gln Leu
355 360 365
Asp Val Gly Asn Asn Pro Arg Val Gly Thr Lys Arg Tyr Met Ala Pro
370 375 380
Glu Val Leu Asp Glu Thr Ile Gln Val Asp Cys Phe Asp Ser Tyr Lys
385 390 395 400
Arg Val Asp Ile Trp Ala Phe Gly Leu Val Leu Trp Glu Val Ala Arg
405 410 415
Arg Met Val Ser Asn Gly Ile Val Glu Asp Tyr Lys Pro Pro Phe Tyr
420 425 430
Asp Val Val Pro Asn Asp Pro Ser Phe Glu Asp Met Arg Lys Val Val
435 440 445
Cys Val Asp Gln Gln Arg Pro Asn Ile Pro Asn Arg Trp Phe Ser Asp
450 455 460
Pro Thr Leu Thr Ser Leu Ala Lys Leu Met Lys Glu Cys Trp Tyr Gln
465 470 475 480
Asn Pro Ser Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Thr
485 490 495

Lys Ile Asp Asn Ser Leu Asp Lys Leu Lys Thr Asp Cys
500 505

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2932 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 310..1905

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GCTCCGCGCC GAGGGCTGGA GGATGCGTTC CCTGGGGTCC GGACTTATGA AAATATGCAT 60

CAGTTTAATA CTGTCTTGGA ATTCAATGAGA TGGAAGCATA GGTCAAAGCT GTTGGAGAA 120

AATCAGAACT ACAGTTTTAT CTAGCCACAT CTTGGAGGAG TCGTAAGAAA GCAGTGGGAG 180

TTGAAGTCAT TGTCAAGTGC TTGCGATCTT TTACAAGAAA ATCTCACTGA ATGATAGTCA 240

TTTAAATTGG TGAAGTAGCA AGACCAATTA TTAAAGGTGA CAGTACACAG GAAACATTAC 300

AATTGAACA ATG ACT CAG CTA TAC ATT TAC ATC AGA TTA TTG GGA GCC 348
Met Thr Gln Leu Tyr Ile Tyr Ile Arg Leu Leu Gly Ala

1

5

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TAT TTG TTC ATC ATT TCT CGT GTT CAA GGA CAG AAT CTG GAT AGT ATG 396
Tyr Leu Phe Ile Ile Ser Arg Val Gln Gly Gln Asn Leu Asp Ser Met
15 20 25

CTT CAT GGC ACT GGG ATG AAA TCA GAC TCC GAC CAG AAA AAG TCA GAA 444
Leu His Gly Thr Gly Met Lys Ser Asp Ser Asp Gln Lys Lys Ser Glu
30 35 40 45

AAT GGA GTA ACC TTA GCA CCA GAG GAT ACC TTG CCT TTT TTA AAG TGC 492
Asn Gly Val Thr Leu Ala Pro Glu Asp Thr Leu Pro Phe Leu Lys Cys
50 55 60

TAT TGC TCA GGG CAC TGT CCA GAT GAT GCT ATT AAT AAC ACA TGC ATA Tyr Cys Ser Gly His Cys Pro Asp Asp Ala Ile Asn Asn Thr Cys Ile 65 70 75	540
ACT AAT GGA CAT TGC TTT GCC ATC ATA GAA GAA GAT GAC CAG GGA GAA Thr Asn Gly His Cys Phe Ala Ile Ile Glu Glu Asp Asp Gln Gly Glu 80 85 90	588
ACC ACA TTA GCT TCA GGG TGT ATG AAA TAT GAA GGA TCT GAT TTT CAG Thr Thr Leu Ala Ser Gly Cys Met Lys Tyr Glu Gly Ser Asp Phe Gln 95 100 105	636
TGC AAA GAT TCT CCA AAA GCC CAG CTA CGC CGG ACA ATA GAA TGT TGT Cys Lys Asp Ser Pro Lys Ala Gln Leu Arg Arg Thr Ile Glu Cys Cys 110 115 120 125	684
CGG ACC AAT TTA TGT AAC CAG TAT TTG CAA CCC ACA CTG CCC CCT GTT Arg Thr Asn Leu Cys Asn Gln Tyr Leu Gln Pro Thr Leu Pro Pro Val 130 135 140	732
GTC ATA GGT CCG TTT TTT GAT GGC AGC ATT CGA TGG CTG GTT TTG CTC Val Ile Gly Pro Phe Phe Asp Gly Ser Ile Arg Trp Leu Val Leu Leu 145 150 155	780
ATT TCT ATG GCT GTC TGC ATA ATT GCT ATG ATC ATC TTC TCC AGC TGC Ile Ser Met Ala Val Cys Ile Ile Ala Met Ile Ile Phe Ser Ser Cys 160 165 170	828
TTT TGT TAC AAA CAT TAT TGC AAG AGC ATC TCA AGC AGA CGT CGT TAC Phe Cys Tyr Lys His Tyr Cys Lys Ser Ile Ser Ser Arg Arg Arg Tyr 175 180 185	876
AAT CGT GAT TTG GAA CAG GAT GAA GCA TTT ATT CCA GTT GGA GAA TCA Asn Arg Asp Leu Glu Gln Asp Glu Ala Phe Ile Pro Val Gly Glu Ser 190 195 200 205	924
CTA AAA GAC CTT ATT GAC CAG TCA CAA AGT TCT GGT AGT GGG TCT GGA Leu Lys Asp Leu Ile Asp Gln Ser Gln Ser Ser Gly Ser Gly Ser Gly 210 215 220	972
CTA CCT TTA TTG GTT CAG CGA ACT ATT GCC AAA CAG ATT CAG ATG GTC Leu Pro Leu Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met Val 225 230 235	1020
CGG CAA GTT GGT AAA GGC CGA TAT GGA GAA GTA TGG ATG GGC AAA TGG Arg Gln Val Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys Trp 240 245 250	1068
CGT GGC GAA AAA GTG GCG GTG AAA GTA TTC TTT ACC ACT GAA GAA GCC Arg Gly Glu Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu Ala 255 260 265	1116

AGC TGG TTT CGA GAA ACA GAA ATC TAC CAA ACT GTG CTA ATG CGC CAT Ser Trp Phe Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg His 270 275 280 285	1164
GAA AAC ATA CTT GGT TTC ATA GCG GCA GAC ATT AAA GGT ACA GGT TCC Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly Ser 290 295 300	1212
TGG ACT CAG CTC TAT TTG ATT ACT GAT TAC CAT GAA AAT GGA TCT CTC Trp Thr Gln Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser Leu 305 310 315	1260
TAT GAC TTC CTG AAA TGT GCT ACA CTG GAC ACC AGA GCC CTG CTT AAA Tyr Asp Phe Leu Lys Cys Ala Thr Leu Asp Thr Arg Ala Leu Leu Lys 320 325 330	1308
TTG GCT TAT TCA GCT GCC TGT GGT CTG TGC CAC CTG CAC ACA GAA ATT Leu Ala Tyr Ser Ala Ala Cys Gly Leu Cys His Leu His Thr Glu Ile 335 340 345	1356
TAT GGC ACC CAA GGA AAG CCC GCA ATT GCT CAT CGA GAC CTA AAG AGC Tyr Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser 350 355 360 365	1404
AAA AAC ATC CTC ATC AAG AAA AAT GGG AGT TGC TGC ATT GCT GAC CTG Lys Asn Ile Leu Ile Lys Lys Asn Gly Ser Cys Cys Ile Ala Asp Leu 370 375 380	1452
GGC CTT GCT GTT AAA TTC AAC AGT GAC ACA AAT GAA GTT GAT GTG CCC Gly Leu Ala Val Lys Phe Asn Ser Asp Thr Asn Glu Val Asp Val Pro 385 390 395	1500
TTG AAT ACC AGG GTG GGC ACC AAA CGC TAC ATG GCT CCC GAA GTG CTG Leu Asn Thr Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu 400 405 410	1548
GAC GAA AGC CTG AAC AAA AAC CAC TTC CAG CCC TAC ATC ATG GCT GAC Asp Glu Ser Leu Asn Lys Asn His Phe Gln Pro Tyr Ile Met Ala Asp 415 420 425	1596
ATC TAC AGC TTC GGC CTA ATC ATT TGG GAG ATG GCT CGT CGT TGT ATC Ile Tyr Ser Phe Gly Leu Ile Ile Trp Glu Met Ala Arg Arg Cys Ile 430 435 440 445	1644
ACA GGA GGG ATC GTG GAA GAA TAC CAA TTG CCA TAT TAC AAC ATG GTA Thr Gly Gly Ile Val Glu Glu Tyr Gln Leu Pro Tyr Tyr Asn Met Val 450 455 460	1692
CCG AGT GAT CCG TCA TAC GAA GAT ATG CGT GAG GTT GTG TGT GTC AAA Pro Ser Asp Pro Ser Tyr Glu Asp Met Arg Glu Val Val Cys Val Lys 465 470 475	1740

CGT TTG CGG CCA ATT GTG TCT AAT CGG TGG AAC AGT GAT GAA TGT CTA Arg Leu Arg Pro Ile Val Ser Asn Arg Trp Asn Ser Asp Glu Cys Leu 480 485 490	1788
CGA GCA GTT TTG AAG CTA ATG TCA GAA TGC TGG GCC CAC AAT CCA GCC Arg Ala Val Leu Lys Leu Met Ser Glu Cys Trp Ala His Asn Pro Ala 495 500 505	1836
TCC AGA CTC ACA GCA TTG AGA ATT AAG AAG ACG CTT GCC AAG ATG GTT Ser Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Ala Lys Met Val 510 515 520 525	1884
GAA TCC CAA GAT GTA AAA ATC TGATGGTTAA ACCATCGGAG GAGAAACTCT Glu Ser Gln Asp Val Lys Ile 530	1935
AGACTGCAAG AACTGTTTT ACCCATGGCA TGGGTGGAAT TAGAGTGGAA TAAGGATGTT	1995
AACTTGGTTC TCAGACTCTT TCTTCACTAC GTGTTCACAG GCTGCTAATA TTAAACCTTT	2055
CAGTACTCTT ATTAGGATAC AAGCTGGAA CTTCTAAACA CTTCATTCTT TATATATGGA	2115
CAGCTTTATT TTAAATGTGG TTTTGATGC CTTTTTTAA GTGGGTTTTT ATGAACTGCA	2175
TCAAGACTTC AATCCTGATT AGTGTCTCCA GTCAAGCTCT GGGTACTGAA TTGCCTGTT	2235
ATAAAACGGT GCTTCTGTG AAAGCCTAA GAAGATAAAT GAGCGCAGCA GAGATGGAGA	2295
AATAGACTTT GCCTTTTACC TGAGACATTC AGTCGTTG TATTCTACCT TTGTAAAACA	2355
GCCTATAGAT GATGATGTGT TTGGGATACT GCTTATTTA TGATAGTTG TCCTGTGTCC	2415
TTAGTGATGT GTGTGTGTCT CCATGCACAT GCACGCCGGG ATTCCCTCTGC TGCCATTG	2475
ATTAGAAGAA AATAATTAT ATGCATGCAC AGGAAGATAT TGGTGGCCGG TGGTTTGTG	2535
CTTTAAAAAT GCAATATCTG ACCAAGATTG GCCAATCTCA TACAAGCCAT TTACTTGCA	2595
AGTGAGATAG CTTCCCCACC AGCTTTATT TTTAACATGA AAGCTGATGC CAAGGCCAAA	2655
AGAAGTTAA AGCATCTGTA AATTGGACT GTTTCCCTTC AACCAACCATT TTTTTGTGG	2715
TTATTATTT TGTCACGGAA AGCATCCTCT CCAAAGTTGG AGCTTCTATT GCCATGAACC	2775
ATGCTTACAA AGAAAGCACT TCTTATTGAA GTGAATTCT GCATTTGATA GCAATGTAAG	2835
TGCCTATAAC CATGTTCTAT ATTCTTTATT CTCAGTAAC TTTAAAAGGG AAGTTATTAA	2895
TATTTGTGT ATAATGTGCT TTATTTGCAA ATCACCC	2932

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 532 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Thr Gln Leu Tyr Ile Tyr Ile Arg Leu Leu Gly Ala Tyr Leu Phe
1 5 10 15
Ile Ile Ser Arg Val Gln Gly Gln Asn Leu Asp Ser Met Leu His Gly
20 25 30
Thr Gly Met Lys Ser Asp Ser Asp Gln Lys Lys Ser Glu Asn Gly Val
35 40 45
Thr Leu Ala Pro Glu Asp Thr Leu Pro Phe Leu Lys Cys Tyr Cys Ser
50 55 60
Gly His Cys Pro Asp Asp Ala Ile Asn Asn Thr Cys Ile Thr Asn Gly
65 70 75 80
His Cys Phe Ala Ile Ile Glu Glu Asp Asp Gln Gly Glu Thr Thr Leu
85 90 95
Ala Ser Gly Cys Met Lys Tyr Glu Gly Ser Asp Phe Gln Cys Lys Asp
100 105 110
Ser Pro Lys Ala Gln Leu Arg Arg Thr Ile Glu Cys Cys Arg Thr Asn
115 120 125
Leu Cys Asn Gln Tyr Leu Gln Pro Thr Leu Pro Pro Val Val Ile Gly
130 135 140
Pro Phe Phe Asp Gly Ser Ile Arg Trp Leu Val Leu Leu Ile Ser Met
145 150 155 160
Ala Val Cys Ile Ile Ala Met Ile Ile Phe Ser Ser Cys Phe Cys Tyr
165 170 175
Lys His Tyr Cys Lys Ser Ile Ser Ser Arg Arg Arg Tyr Asn Arg Asp
180 185 190
Leu Glu Gln Asp Glu Ala Phe Ile Pro Val Gly Glu Ser Leu Lys Asp
195 200 205
Leu Ile Asp Gln Ser Gln Ser Ser Gly Ser Gly Leu Pro Leu
210 215 220
Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met Val Arg Gln Val
225 230 235 240
Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys Trp Arg Gly Glu
245 250 255
Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu Ala Ser Trp Phe
260 265 270
Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg His Glu Asn Ile
275 280 285
Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly Ser Trp Thr Gln
290 295 300
Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser Leu Tyr Asp Phe
305 310 315 320
Leu Lys Cys Ala Thr Leu Asp Thr Arg Ala Leu Leu Lys Leu Ala Tyr
325 330 335
Ser Ala Ala Cys Gly Leu Cys His Leu His Thr Glu Ile Tyr Gly Thr
340 345 350
Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Lys Asn Ile
355 360 365

Leu Ile Lys Lys Asn Gly Ser Cys Cys Ile Ala Asp Leu Gly Leu Ala
 370 375 380
 Val Lys Phe Asn Ser Asp Thr Asn Glu Val Asp Val Pro Leu Asn Thr
 385 390 395 400
 Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Ser
 405 410 415
 Leu Asn Lys Asn His Phe Gln Pro Tyr Ile Met Ala Asp Ile Tyr Ser
 420 425 430
 Phe Gly Leu Ile Ile Trp Glu Met Ala Arg Arg Cys Ile Thr Gly Gly
 435 440 445
 Ile Val Glu Glu Tyr Gln Leu Pro Tyr Tyr Asn Met Val Pro Ser Asp
 450 455 460
 Pro Ser Tyr Glu Asp Met Arg Glu Val Val Cys Val Lys Arg Leu Arg
 465 470 475 480
 Pro Ile Val Ser Asn Arg Trp Asn Ser Asp Glu Cys Leu Arg Ala Val
 485 490 495
 Leu Lys Leu Met Ser Glu Cys Trp Ala His Asn Pro Ala Ser Arg Leu
 500 505 510
 Thr Ala Leu Arg Ile Lys Lys Thr Leu Ala Lys Met Val Glu Ser Gln
 515 520 525
 Asp Val Lys Ile
 530

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1515

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

ATG GCG GAG TCG GCC GGA GCC TCC TCC TTC TTC CCC CTT GTT GTC CTC
 Met Ala Glu Ser Ala Gly Ala Ser Ser Phe Phe Pro Leu Val Val Leu

1

5

10

15

48

CTG CTC GCC GGC AGC GGC GGG TCC GGG CCC CGG GGG GTC CAG GCT CTG Leu Leu Ala Gly Ser Gly Ser Gly Pro Arg Gly Val Gln Ala Leu 20 25 30	96
CTG TGT GCG TGC ACC AGC TGC CTC CAG GCC AAC TAC ACG TGT GAG ACA Leu Cys Ala Cys Thr Ser Cys Leu Gln Ala Asn Tyr Thr Cys Glu Thr 35 40 45	144
GAT GGG GCC TGC ATG GTT TCC TTT TTC AAT CTG GAT GGG ATG GAG CAC Asp Gly Ala Cys Met Val Ser Phe Phe Asn Leu Asp Gly Met Glu His 50 55 60	192
CAT GTG CGC ACC TGC ATC CCC AAA GTG GAG CTG GTC CCT GCC GGG AAG His Val Arg Thr Cys Ile Pro Lys Val Glu Leu Val Pro Ala Gly Lys 65 70 75 80	240
CCC TTC TAC TGC CTG AGC TCG GAG GAC CTG CGC AAC ACC CAC TGC TGC Pro Phe Tyr Cys Leu Ser Ser Glu Asp Leu Arg Asn Thr His Cys Cys 85 90 95	288
TAC ACT GAC TAC TGC AAC AGG ATC GAC TTG AGG GTG CCC AGT GGT CAC Tyr Thr Asp Tyr Cys Asn Arg Ile Asp Leu Arg Val Pro Ser Gly His 100 105 110	336
CTC AAG GAG CCT GAG CAC CCG TCC ATG TGG GGC CCG GTG GAG CTG GTA Leu Lys Glu Pro Glu His Pro Ser Met Trp Gly Pro Val Glu Leu Val 115 120 125	384
GGC ATC ATC GCC GGC CCG GTG TTC CTC CTG TTC CTC ATC ATC ATC ATT Gly Ile Ile Ala Gly Pro Val Phe Leu Leu Phe Leu Ile Ile Ile Ile 130 135 140	432
GTT TTC CTT GTC ATT AAC TAT CAT CAG CGT GTC TAT CAC AAC CGC CAG Val Phe Leu Val Ile Asn Tyr His Gln Arg Val Tyr His Asn Arg Gln 145 150 155 160	480
AGA CTG GAC ATG GAA GAT CCC TCA TGT GAG ATG TGT CTC TCC AAA GAC Arg Leu Asp Met Glu Asp Pro Ser Cys Glu Met Cys Leu Ser Lys Asp 165 170 175	528
AAG ACG CTC CAG GAT CTT GTC TAC GAT CTC TCC ACC TCA GGG TCT GGC Lys Thr Leu Gln Asp Leu Val Tyr Asp Leu Ser Thr Ser Gly Ser Gly 180 185 190	576
TCA GGG TTA CCC CTC TTT GTC CAG CGC ACA GTG GCC CGA ACC ATC GTT Ser Gly Leu Pro Leu Phe Val Gln Arg Thr Val Ala Arg Thr Ile Val 195 200 205	624
TTA CAA GAG ATT ATT GGC AAG GGT CGG TTT GGG GAA GTA TGG CGG GGC Leu Gln Glu Ile Ile Gly Lys Gly Arg Phe Gly Glu Val Trp Arg Gly 210 215 220	672

CGC TGG AGG GGT GGT GAT GTG GCT GTG AAA ATA TTC TCT TCT CGT GAA Arg Trp Arg Gly Gly Asp Val Ala Val Lys Ile Phe Ser Ser Arg Glu 225 230 235 240	720
GAA CGG TCT TGG TTC AGG GAA GCA GAG ATA TAC CAG ACG GTC ATG CTG Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr Val Met Leu 245 250 255	768
CGC CAT GAA AAC ATC CTT GGA TTT ATT GCT GCT GAC AAT AAA GAT AAT Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Asn Lys Asp Asn 260 265 270	816
GGC ACC TGG ACA CAG CTG TGG CTT GTT TCT GAC TAT CAT GAG CAC GGG Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Asp Tyr His Glu His Gly 275 280 285	864
TCC CTG TTT GAT TAT CTG AAC CGG TAC ACA GTG ACA ATT GAG GGG ATG Ser Leu Phe Asp Tyr Leu Asn Arg Tyr Thr Val Thr Ile Glu Gly Met 290 295 300	912
ATT AAG CTG GCC TTG TCT GCT GCT AGT GGG CTG GCA CAC CTG CAC ATG Ile Lys Leu Ala Leu Ser Ala Ala Ser Gly Leu Ala His Leu His Met 305 310 315 320	960
GAG ATC GTG GGC ACC CAA GGG AAG CCT GGA ATT GCT CAT CGA GAC TTA Glu Ile Val Gly Thr Gln Gly Lys Pro Gly Ile Ala His Arg Asp Leu 325 330 335	1008
AAG TCA AAG AAC ATT CTG GTG AAG AAA AAT GGC ATG TGT GCC ATA GCA Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Met Cys Ala Ile Ala 340 345 350	1056
GAC CTG GGC CTG GCT GTC CGT CAT GAT GCA GTC ACT GAC ACC ATT GAC Asp Leu Gly Leu Ala Val Arg His Asp Ala Val Thr Asp Thr Ile Asp 355 360 365	1104
ATT GCC CCG AAT CAG AGG GTG GGG ACC AAA CGA TAC ATG GCC CCT GAA Ile Ala Pro Asn Gln Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu 370 375 380	1152
GTA CTT GAT GAA ACC ATT AAT ATG AAA CAC TTT GAC TCC TTT AAA TGT Val Leu Asp Glu Thr Ile Asn Met Lys His Phe Asp Ser Phe Lys Cys 385 390 395 400	1200
GCT GAT ATT TAT GCC CTC GGG CTT GTA TAT TGG GAG ATT GCT CGA AGA Ala Asp Ile Tyr Ala Leu Gly Leu Val Tyr Trp Glu Ile Ala Arg Arg 405 410 415	1248
TGC AAT TCT GGA GGA GTC CAT GAA GAA TAT CAG CTG CCA TAT TAC GAC Cys Asn Ser Gly Gly Val His Glu Glu Tyr Gln Leu Pro Tyr Tyr Asp 420 425 430	1296
TTA GTG CCC TCT GAC CCT TCC ATT GAG GAA ATG CGA AAG GTT GTA TGT Leu Val Pro Ser Asp Pro Ser Ile Glu Glu Met Arg Lys Val Val Cys 435 440 445	1344

GAT CAG AAG CTG CGT CCC AAC ATC CCC AAC TGG TGG CAG AGT TAT GAG Asp Gln Lys Leu Arg Pro Asn Ile Pro Asn Trp Trp Gln Ser Tyr Glu 450 455 460	1392
GCA CTG CGG GTG ATG GGG AAG ATG ATG CGA GAG TGT TGG TAT GCC AAC Ala Leu Arg Val Met Gly Lys Met Met Arg Glu Cys Trp Tyr Ala Asn 465 470 475 480	1440
GGC GCA GCC CGC CTG ACG GCC CTG CGC ATC AAG AAG ACC CTC TCC CAG Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Ser Gln 485 490 495	1488
CTC AGC GTG CAG GAA GAC GTG AAG ATC TAACTGCTCC CTCTCTCCAC Leu Ser Val Gln Glu Asp Val Lys Ile 500 505	1535
ACGGAGCTCC TGGCAGCGAG AACTACGCAC AGCTGCCGCG TTGAGCGTAC GATGGAGGCC	1595
TACCTCTCGT TTCTGCCAG CCCTCTGTGG CCAGGAGCCC TGGCCCGCAA GAGGGACAGA	1655
GCCCAGGAGA GACTCGCTCA CTCCCATGTT GGGTTTGAGA CAGACACCTT TTCTATTTAC	1715
CTCCTAATGG CATGGAGACT CTGAGAGCGA ATTGTGTGGA GAACTCAGTG CCACACCTCG	1775
AACTGGTTGT AGTGGGAAGT CCCGCGAAAC CCGGTGCATC TGGCACGTGG CCAGGAGCCA	1835
TGACAGGGGC GCTTGGGAGG GGCCGGAGGA ACCGAGGTGT TGCCAGTGCT AAGCTGCCCT	1895
GAGGGTTTCC TTCGGGGACC AGCCCACAGC ACACCAAGGT GGCCCGGAAG AACCAGAAGT	1955
GCAGCCCCCTC TCACAGGCAG CTCTGAGCCG CGCTTCCCCC TCCTCCCTGG GATGGACGCT	2015
GCCGGGAGAC TGCCAGTGGA GACGGAATCT GCGCCTTGT CTGTCCAGCC GTGTGTGCAT	2075
GTGCCGAGGT GCGTCCCCCG TTGTGCCTGG TTCGTGCCAT GCCCTTACAC GTGCGTGTGA	2135
GTGTGTGTGT GTGTCTGTAG GTGCGCACTT ACCTGCTTGA GCTTTCTGTG CATGTGCAGG	2195
TCGGGGGTGT GGTCGTCATG CTGTCCGTGC TTGCTGGTGC CTCTTTCAAG TAGTGAGCAG	2255
CATCTAGTTT CCCTGGTGCC CTTCCCTGGA GGTCTCTCCC TCCCCCAGAG CCCCTCATGC CACAGTGGTA CTCTGTGT	2315 2333

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met Ala Glu Ser Ala Gly Ala Ser Ser Phe Phe Pro Leu Val Val Leu
1 5 10 15
Leu Leu Ala Gly Ser Gly Ser Gly Pro Arg Gly Val Gln Ala Leu
20 25 30
Leu Cys Ala Cys Thr Ser Cys Leu Gln Ala Asn Tyr Thr Cys Glu Thr
35 40 45
Asp Gly Ala Cys Met Val Ser Phe Phe Asn Leu Asp Gly Met Glu His
50 55 60
His Val Arg Thr Cys Ile Pro Lys Val Glu Leu Val Pro Ala Gly Lys
65 70 75 80
Pro Phe Tyr Cys Leu Ser Ser Glu Asp Leu Arg Asn Thr His Cys Cys
85 90 95
Tyr Thr Asp Tyr Cys Asn Arg Ile Asp Leu Arg Val Pro Ser Gly His
100 105 110
Leu Lys Glu Pro Glu His Pro Ser Met Trp Gly Pro Val Glu Leu Val
115 120 125
Gly Ile Ile Ala Gly Pro Val Phe Leu Leu Phe Leu Ile Ile Ile
130 135 140
Val Phe Leu Val Ile Asn Tyr His Gln Arg Val Tyr His Asn Arg Gln
145 150 155 160
Arg Leu Asp Met Glu Asp Pro Ser Cys Glu Met Cys Leu Ser Lys Asp
165 170 175
Lys Thr Leu Gln Asp Leu Val Tyr Asp Leu Ser Thr Ser Gly Ser Gly
180 185 190
Ser Gly Leu Pro Leu Phe Val Gln Arg Thr Val Ala Arg Thr Ile Val
195 200 205
Leu Gln Glu Ile Ile Gly Lys Gly Arg Phe Gly Glu Val Trp Arg Gly
210 215 220
Arg Trp Arg Gly Gly Asp Val Ala Val Lys Ile Phe Ser Ser Arg Glu
225 230 235 240
Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr Val Met Leu
245 250 255
Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Asn Lys Asp Asn
260 265 270
Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Asp Tyr His Glu His Gly
275 280 285
Ser Leu Phe Asp Tyr Leu Asn Arg Tyr Thr Val Thr Ile Glu Gly Met
290 295 300
Ile Lys Leu Ala Leu Ser Ala Ala Ser Gly Leu Ala His Leu His Met
305 310 315 320
Glu Ile Val Gly Thr Gln Gly Lys Pro Gly Ile Ala His Arg Asp Leu
325 330 335
Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Met Cys Ala Ile Ala
340 345 350
Asp Leu Gly Leu Ala Val Arg His Asp Ala Val Thr Asp Thr Ile Asp
355 360 365
Ile Ala Pro Asn Gln Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu
370 375 380
Val Leu Asp Glu Thr Ile Asn Met Lys His Phe Asp Ser Phe Lys Cys
385 390 395 400
Ala Asp Ile Tyr Ala Leu Gly Leu Val Tyr Trp Glu Ile Ala Arg Arg
405 410 415
Cys Asn Ser Gly Gly Val His Glu Glu Tyr Gln Leu Pro Tyr Tyr Asp
420 425 430

Leu	Val	Pro	Ser	Asp	Pro	Ser	Ile	Glu	Glu	Met	Arg	Lys	Val	Val	Cys
435							440					445			
Asp	Gln	Lys	Leu	Arg	Pro	Asn	Ile	Pro	Asn	Trp	Trp	Gln	Ser	Tyr	Glu
450							455					460			
Ala	Leu	Arg	Val	Met	Gly	Lys	Met	Met	Arg	Glu	Cys	Trp	Tyr	Ala	Asn
465							470				475				480
Gly	Ala	Ala	Arg	Leu	Thr	Ala	Leu	Arg	Ile	Lys	Lys	Thr	Leu	Ser	Gln
							485			490				495	
Leu	Ser	Val	Gln	Glu	Asp	Val	Lys	Ile							
							500			505					

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mouse

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 77..1585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GGCGAGGCAGA	GGTTTGCTGG	GGTGAGGCAG	CGGCGCGGCC	GGGCCGGGCC	GGGCCACAGG	60
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CGGTGGCGGC	GGGACC	ATG	GAG	GCG	GCG	GTC	GCT	GCT	CCG	CGT	CCC	CGG	109
		Met	Glu	Ala	Ala	Val	Ala	Ala	Pro	Arg	Pro	Arg	
		1				5				10			

CTG	CTC	CTC	CTC	GTG	CTG	GCG	CTG	157						
Leu	Leu	Leu	Leu	Val	Leu	Ala	Leu							
						15		20		25				

CTC	CCG	GGG	GCG	ACG	GCG	TTA	CAG	TGT	TTC	TGC	CAC	CTC	TGT	ACA	AAA	205
Leu	Pro	Gly	Ala	Thr	Ala	Leu	Gln	Cys	Phe	Cys	His	Leu	Cys	Thr	Lys	
							30		35		40					

GAC	AAT	TTT	ACT	TGT	GTG	ACA	GAT	GGG	CTC	TGC	TTT	GTC	TCT	GTC	ACA	253
Asp	Asn	Phe	Thr	Cys	Val	Thr	Asp	Gly	Leu	Cys	Phe	Val	Ser	Val	Thr	
							45		50		55					

GAG ACC ACA GAC AAA GTT ATA CAC AAC AGC ATG TGT ATA GCT GAA ATT Glu Thr Thr Asp Lys Val Ile His Asn Ser Met Cys Ile Ala Glu Ile 60 65 70 75	301
GAC TTA ATT CCT CGA GAT AGG CCG TTT GTA TGT GCA CCC TCT TCA AAA Asp Leu Ile Pro Arg Asp Arg Pro Phe Val Cys Ala Pro Ser Ser Lys 80 85 90	349
ACT GGG TCT GTG ACT ACA ACA TAT TGC TGC AAT CAG GAC CAT TGC AAT Thr Gly Ser Val Thr Thr Tyr Cys Cys Asn Gln Asp His Cys Asn 95 100 105	397
AAA ATA GAA CTT CCA ACT ACT GTA AAG TCA TCA CCT GGC CTT GGT CCT Lys Ile Glu Leu Pro Thr Thr Val Lys Ser Ser Pro Gly Leu Gly Pro 110 115 120	445
GTG GAA CTG GCA GCT GTC ATT GCT GGA CCA GTG TGC TTC GTC TGC ATC Val Glu Leu Ala Ala Val Ile Ala Gly Pro Val Cys Phe Val Cys Ile 125 130 135	493
TCA CTC ATG TTG ATG GTC TAT ATC TGC CAC AAC CGC ACT GTC ATT CAC Ser Leu Met Leu Met Val Tyr Ile Cys His Asn Arg Thr Val Ile His 140 145 150 155	541
CAT CGA GTG CCA AAT GAA GAG GAC CCT TCA TTA GAT CGC CCT TTT ATT His Arg Val Pro Asn Glu Glu Asp Pro Ser Leu Asp Arg Pro Phe Ile 160 165 170	589
TCA GAG GGT ACT ACG TTG AAA GAC TTA ATT TAT GAT ATG ACA ACG TCA Ser Glu Gly Thr Thr Leu Lys Asp Leu Ile Tyr Asp Met Thr Thr Ser 175 180 185	637
GGT TCT GGC TCA GGT TTA CCA TTG CTT GTT CAG AGA ACA ATT GCG AGA Gly Ser Gly Ser Gly Leu Pro Leu Leu Val Gln Arg Thr Ile Ala Arg 190 195 200	685
ACT ATT GTG TTA CAA GAA AGC ATT GGC AAA GGT CGA TTT GGA GAA GTT Thr Ile Val Leu Gln Glu Ser Ile Gly Lys Gly Arg Phe Gly Glu Val 205 210 215	733
TGG AGA GGA AAG TGG CGG GGA GAA GAA GTT GCT GTT AAG ATA TTC TCC Trp Arg Gly Lys Trp Arg Gly Glu Glu Val Ala Val Lys Ile Phe Ser 220 225 230 235	781
TCT AGA GAA GAA CGT TCG TGG TTC CGT GAG GCA GAG ATT TAT CAA ACT Ser Arg Glu Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr 240 245 250	829
GTA ATG TTA CGT CAT GAA AAC ATC CTG GGA TTT ATA GCA GCA GAC AAT Val Met Leu Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Asn 255 260 265	877

AAA GAC AAT GGT ACT TGG ACT CAG CTC TGG TTG GTG TCA GAT TAT CAT Lys Asp Asn Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Asp Tyr His 270 275 280	925
GAG CAT GGA TCC CTT TTT GAT TAC TTA AAC AGA TAC ACA GTT ACT GTG Glu His Gly Ser Leu Phe Asp Tyr Leu Asn Arg Tyr Thr Val Thr Val 285 290 295	973
GAA GGA ATG ATA AAA CTT GCT CTG TCC ACG GCG AGC GGT CTT GCC CAT Glu Gly Met Ile Lys Leu Ala Leu Ser Thr Ala Ser Gly Leu Ala His 300 305 310 315	1021
CTT CAC ATG GAG ATT GTT GGT ACC CAA GGA AAG CCA GCC ATT GCT CAT Leu His Met Glu Ile Val Gly Thr Gln Gly Lys Pro Ala Ile Ala His 320 325 330	1069
AGA GAT TTG AAA TCA AAG AAT ATC TTG GTA AAG AAG AAT GGA ACT TGC Arg Asp Leu Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Thr Cys 335 340 345	1117
TGT ATT GCA GAC TTA GGA CTG GCA GTA AGA CAT GAT TCA GCC ACA GAT Cys Ile Ala Asp Leu Gly Leu Ala Val Arg His Asp Ser Ala Thr Asp 350 355 360	1165
ACC ATT GAT ATT GCT CCA AAC CAC AGA GTG GGA ACA AAA AGG TAC ATG Thr Ile Asp Ile Ala Pro Asn His Arg Val Gly Thr Lys Arg Tyr Met 365 370 375	1213
GCC CCT GAA GTT CTC GAT GAT TCC ATA AAT ATG AAA CAT TTT GAA TCC Ala Pro Glu Val Leu Asp Asp Ser Ile Asn Met Lys His Phe Glu Ser 380 385 390 395	1261
TTC AAA CGT GCT GAC ATC TAT GCA ATG GGC TTA GTA TTC TGG GAA ATT Phe Lys Arg Ala Asp Ile Tyr Ala Met Gly Leu Val Phe Trp Glu Ile 400 405 410	1309
GCT CGA CGA TGT TCC ATT GGT GGA ATT CAT GAA GAT TAC CAA CTG CCT Ala Arg Arg Cys Ser Ile Gly Gly Ile His Glu Asp Tyr Gln Leu Pro 415 420 425	1357
TAT TAT GAT CTT GTA CCT TCT GAC CCA TCA GTT GAA GAA ATG AGA AAA Tyr Tyr Asp Leu Val Pro Ser Asp Pro Ser Val Glu Glu Met Arg Lys 430 435 440	1405
GTT GTT TGT GAA CAG AAG TTA AGG CCA AAT ATC CCA AAC AGA TGG CAG Val Val Cys Glu Gln Lys Leu Arg Pro Asn Ile Pro Asn Arg Trp Gln 445 450 455	1453
AGC TGT GAA GCC TTG AGA GTA ATG GCT AAA ATT ATG AGA GAA TGT TGG Ser Cys Glu Ala Leu Arg Val Met Ala Lys Ile Met Arg Glu Cys Trp 460 465 470 475	1501

TAT GCC AAT GGA GCA GCT AGG CTT ACA GCA TTG CGG ATT AAG AAA ACA	1549
Tyr Ala Asn Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr	
480 485 490	
TTA TCG CAA CTC AGT CAA CAG GAA GGC ATC AAA ATG TAATTCTACA	1595
Leu Ser Gln Leu Ser Gln Gln Glu Gly Ile Lys Met	
495 500	
GCTTTGCCTG AACTCTCCTT TTTTCTTCAG ATCTGCTCCT GGGTTTTAAT TTGGGAGGTC	1655
AGTTGTTCTA CCTCACTGAG AGGGAACAGA AGGATATTGC TTCCCTTTGC AGCAGTGTAA	1715
TAAAGTCAAT TAAAAACTTC CCAGGATTTC TTTGGACCCA GGAAACAGCC ATGTGGGTCC	1775
TTTCTGTGCA CTATGAACGC TTCTTCCC GGACAGAAAA TGTGTAGTCT ACCTTTATTT	1835
TTTATTAACA AAACTTGTTT TTTAAAAGA TGATTGCTGG TCTTAACCTT AGGTAACTCT	1895
GCTGTGCTGG AGATCATCTT TAAGGGCAA GGAGTTGGAT TGCTGAATTA CAATGAAACA	1955
TGTCTTATTA CTAAAGAAAG TGATTTACTC CTGGTTAGTA CATTCTCAGA GGATTCTGAA	2015
CCACTAGAGT TTCCTTGATT CAGACTTGA ATGTACTGTT CTATAGTTT TCAGGATCTT	2075
AAAACTAACA CTTATAAAC TCTTATCTT AGTCTAAAAA TGACCTCATA TAGTAGTGAG	2135
GAACATAATT CATGCAATTG TATTTGTAT ACTATTATTG TTCTTTCACT TATTCAGAAC	2195
ATTACATGCC TTCAAAATGG GATTGTACTA TACCAGTAAG TGCCACTTCT GTGTCTTCT	2255
AATGGAAATG AGTAGAATTG CTGAAAGTCT CTATGTTAAA ACCTATAGTG TTT	2308

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 503 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met	Glu	Ala	Ala	Val	Ala	Ala	Pro	Arg	Pro	Arg	Leu	Leu	Leu	Leu	Val
1				5			10				15				
Leu	Ala	Leu	Leu	Pro	Gly	Ala	Thr								
					20		25			30					
Ala	Leu	Gln	Cys	Phe	Cys	His	Leu	Cys	Thr	Lys	Asp	Asn	Phe	Thr	Cys
					35		40			45					
Val	Thr	Asp	Gly	Leu	Cys	Phe	Val	Ser	Val	Thr	Glu	Thr	Thr	Asp	Lys
					50		55			60					
Val	Ile	His	Asn	Ser	Met	Cys	Ile	Ala	Glu	Ile	Asp	Leu	Ile	Pro	Arg
					65		70			75			80		
Asp	Arg	Pro	Phe	Val	Cys	Ala	Pro	Ser	Ser	Lys	Thr	Gly	Ser	Val	Thr
					85		90			95					

Thr Thr Tyr Cys Cys Asn Gln Asp His Cys Asn Lys Ile Glu Leu Pro
100 105 110
Thr Thr Val Lys Ser Ser Pro Gly Leu Gly Pro Val Glu Leu Ala Ala
115 120 125
Val Ile Ala Gly Pro Val Cys Phe Val Cys Ile Ser Leu Met Leu Met
130 135 140
Val Tyr Ile Cys His Asn Arg Thr Val Ile His His Arg Val Pro Asn
145 150 155 160
Glu Glu Asp Pro Ser Leu Asp Arg Pro Phe Ile Ser Glu Gly Thr Thr
165 170 175
Leu Lys Asp Leu Ile Tyr Asp Met Thr Thr Ser Gly Ser Gly Ser Gly
180 185 190
Leu Pro Leu Leu Val Gln Arg Thr Ile Ala Arg Thr Ile Val Leu Gln
195 200 205
Glu Ser Ile Gly Lys Gly Arg Phe Gly Glu Val Trp Arg Gly Lys Trp
210 215 220
Arg Gly Glu Glu Val Ala Val Lys Ile Phe Ser Ser Arg Glu Glu Arg
225 230 235 240
Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr Val Met Leu Arg His
245 250 255
Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Asn Lys Asp Asn Gly Thr
260 265 270
Trp Thr Gln Leu Trp Leu Val Ser Asp Tyr His Glu His Gly Ser Leu
275 280 285
Phe Asp Tyr Leu Asn Arg Tyr Thr Val Thr Val Glu Gly Met Ile Lys
290 295 300
Leu Ala Leu Ser Thr Ala Ser Gly Leu Ala His Leu His Met Glu Ile
305 310 315 320
Val Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser
325 330 335
Lys Asn Ile Leu Val Lys Lys Asn Gly Thr Cys Cys Ile Ala Asp Leu
340 345 350
Gly Leu Ala Val Arg His Asp Ser Ala Thr Asp Thr Ile Asp Ile Ala
355 360 365
Pro Asn His Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu
370 375 380
Asp Asp Ser Ile Asn Met Lys His Phe Glu Ser Phe Lys Arg Ala Asp
385 390 395 400
Ile Tyr Ala Met Gly Leu Val Phe Trp Glu Ile Ala Arg Arg Cys Ser
405 410 415
Ile Gly Gly Ile His Glu Asp Tyr Gln Leu Pro Tyr Tyr Asp Leu Val
420 425 430
Pro Ser Asp Pro Ser Val Glu Glu Met Arg Lys Val Val Cys Glu Gln
435 440 445
Lys Leu Arg Pro Asn Ile Pro Asn Arg Trp Gln Ser Cys Glu Ala Leu
450 455 460
Arg Val Met Ala Lys Ile Met Arg Glu Cys Trp Tyr Ala Asn Gly Ala
465 470 475 480
Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Ser Gln Leu Ser
485 490 495
Gln Gln Glu Gly Ile Lys Met
500

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1922 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mouse

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 241..1746

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GAGAGCACAG CCCTTCCCAG TCCCCGGAGC CGCCGCGCCA CGCGCGCATG ATCAAGACCT	60
TTTCCCCGGC CCCACAGGGC CTCTGGACGT GAGACCCCGG CCGCCTCCGC AAGGAGAGGC	120
GGGGGTCGAG TCGCCCTGTC CAAAGGCCTC AATCTAAACA ATCTTGATTC CTGTTGCCGG	180
CTGGCGGGAC CCTGAATGGC AGGAAATCTC ACCACATCTC TTCTCCTATC TCCAAGGACC	240
ATG ACC TTG GGG AGC TTC AGA AGG GGC CTT TTG ATG CTG TCG GTG GCC	288
Met Thr Leu Gly Ser Phe Arg Arg Gly Leu Leu Met Leu Ser Val Ala	
1 5 10 15	
TTG GGC CTA ACC CAG GGG AGA CTT GCG AAG CCT TCC AAG CTG GTG AAC	336
Leu Gly Leu Thr Gln Gly Arg Leu Ala Lys Pro Ser Lys Leu Val Asn	
20 25 30	
TGC ACT TGT GAG AGC CCA CAC TGC AAG AGA CCA TTC TGC CAG GGG TCA	384
Cys Thr Cys Glu Ser Pro His Cys Lys Arg Pro Phe Cys Gln Gly Ser	
35 40 45	
TGG TGC ACA GTG GTG CTG GTT CGA GAG CAG GGC AGG CAC CCC CAG GTC	432
Trp Cys Thr Val Val Leu Val Arg Glu Gln Gly Arg His Pro Gln Val	
50 55 60	
TAT CGG GGC TGT GGG AGC CTG AAC CAG GAG CTC TGC TTG GGA CGT CCC	480
Tyr Arg Gly Cys Gly Ser Leu Asn Gln Glu Leu Cys Leu Gly Arg Pro	
65 70 75 80	

ACG GAG TTT CTG AAC CAT CAC TGC TGC TAT AGA TCC TTC TGC AAC CAC Thr Glu Phe Leu Asn His His Cys Cys Tyr Arg Ser Phe Cys Asn His	85	90	95	528
AAC GTG TCT CTG ATG CTG GAG GCC ACC CAA ACT CCT TCG GAG GAG CCA Asn Val Ser Leu Met Leu Glu Ala Thr Gln Thr Pro Ser Glu Glu Pro	100	105	110	576
GAA GTT GAT GCC CAT CTG CCT CTG ATC CTG GGT CCT GTG CTG GCC TTG Glu Val Asp Ala His Leu Pro Leu Ile Leu Gly Pro Val Leu Ala Leu	115	120	125	624
CCG GTC CTG GTG GCC CTG GGT GCT CTG GGC TTG TGG CGT GTC CGG CGG Pro Val Leu Val Ala Leu Gly Ala Leu Gly Leu Trp Arg Val Arg Arg	130	135	140	672
AGG CAG GAG AAG CAG CGG GAT TTG CAC AGT GAC CTG GGC GAG TCC AGT Arg Gln Glu Lys Gln Arg Asp Leu His Ser Asp Leu Gly Glu Ser Ser	145	150	155	720
CTC ATC CTG AAG GCA TCT GAA CAG GCA GAC AGC ATG TTG GGG GAC TTC Leu Ile Leu Lys Ala Ser Glu Gln Ala Asp Ser Met Leu Gly Asp Phe	165	170	175	768
CTG GAC AGC GAC TGT ACC ACG GGC AGC GGC TCG GGG CTC CCC TTC TTG Leu Asp Ser Asp Cys Thr Thr Gly Ser Gly Leu Pro Phe Leu	180	185	190	816
GTG CAG AGG ACG GTA GCT CGG CAG GTT GCG CTG GTA GAG TGT GTG GGA Val Gln Arg Thr Val Ala Arg Gln Val Ala Leu Val Glu Cys Val Gly	195	200	205	864
AAG GGC CGA TAT GGC GAG GTG TGG CGC GGT TCG TGG CAT GGC GAA AGC Lys Gly Arg Tyr Gly Glu Val Trp Arg Gly Ser Trp His Gly Glu Ser	210	215	220	912
GTG GCG GTC AAG ATT TTC TCC TCA CGA GAT GAG CAG TCC TGG TTC CGG Val Ala Val Lys Ile Phe Ser Ser Arg Asp Glu Gln Ser Trp Phe Arg	225	230	235	960
GAG ACG GAG ATC TAC AAC ACA GTT CTG CTT AGA CAC GAC AAC ATC CTA Glu Thr Glu Ile Tyr Asn Thr Val Leu Leu Arg His Asp Asn Ile Leu	245	250	255	1008
GGC TTC ATC GCC TCC GAC ATG ACT TCG CGG AAC TCG AGC ACG CAG CTG Gly Phe Ile Ala Ser Asp Met Thr Ser Arg Asn Ser Ser Thr Gln Leu	260	265	270	1056
TGG CTC ATC ACC CAC TAC CAT GAA CAC GGC TCC CTC TAT GAC TTT CTG Trp Leu Ile Thr His Tyr His Glu His Gly Ser Leu Tyr Asp Phe Leu	275	280	285	1104

CAG AGG CAG ACG CTG GAG CCC CAG TTG GCC CTG AGG CTA GCT GTG TCC Gln Arg Gln Thr Leu Glu Pro Gln Leu Ala Leu Arg Leu Ala Val Ser 290 295 300	1152
CCG GCC TGC GGC CTG GCG CAC CTA CAT GTG GAG ATC TTT GGC ACT CAA Pro Ala Cys Gly Leu Ala His Leu His Val Glu Ile Phe Gly Thr Gln 305 310 315 320	1200
GGC AAA CCA GCC ATT GCC CAT CGT GAC CTC AAG AGT CGC AAT GTG CTG Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Arg Asn Val Leu 325 330 335	1248
GTC AAG AGT AAC TTG CAG TGT TGC ATT GCA GAC CTG GGA CTG GCT GTG Val Lys Ser Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly Leu Ala Val 340 345 350	1296
ATG CAC TCA CAA AGC AAC GAG TAC CTG GAT ATC GGC AAC ACA CCC CGA Met His Ser Gln Ser Asn Glu Tyr Leu Asp Ile Gly Asn Thr Pro Arg 355 360 365	1344
GTG GGT ACC AAA AGA TAC ATG GCA CCC GAG GTG CTG GAT GAG CAC ATC Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu His Ile 370 375 380	1392
CGC ACA GAC TGC TTT GAG TCG TAC AAG TGG ACA GAC ATC TGG GCC TTT Arg Thr Asp Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala Phe 385 390 395 400	1440
GGC CTA GTG CTA TGG GAG ATC GCC CGG CGG ACC ATC ATC AAT GGC ATT Gly Leu Val Leu Trp Glu Ile Ala Arg Arg Thr Ile Ile Asn Gly Ile 405 410 415	1488
GTG GAG GAT TAC AGG CCA CCT TTC TAT GAC ATG GTA CCC AAT GAC CCC Val Glu Asp Tyr Arg Pro Pro Phe Tyr Asp Met Val Pro Asn Asp Pro 420 425 430	1536
AGT TTT GAG GAC ATG AAA AAG GTG GTG TGC GTT GAC CAG CAG ACA CCC Ser Phe Glu Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr Pro 435 440 445	1584
ACC ATC CCT AAC CGG CTG GCT GCA GAT CCG GTC CTC TCC GGG CTG GCC Thr Ile Pro Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu Ala 450 455 460	1632
CAG ATG ATG AGA GAG TGC TGG TAC CCC AAC CCC TCT GCT CGC CTC ACC Gln Met Met Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu Thr 465 470 475 480	1680
GCA CTG CGC ATA AAG AAG ACA TTG CAG AAG CTC AGT CAC AAT CCA GAG Ala Leu Arg Ile Lys Lys Thr Leu Gln Lys Leu Ser His Asn Pro Glu 485 490 495	1728

AAG CCC AAA GTG ATT CAC TAGCCCAGGG CCACCAGGCT TCCTCTGCCT	1776
Lys Pro Lys Val Ile His	
500	
AAAGTGTGTG CTGGGAAAGA AGACATAGCC TGTCTGGTA GAGGGAGTGA AGAGAGTGTG	1836
CACGCTGCC C TGTGTGTGCC TGCTCAGCTT GCTCCCAGCC CATCCAGCCA AAAATACAGC	1896
TGAGCTGAAA TTCAAAAAAA AAAAAA	1922

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met Thr Leu Gly Ser Phe Arg Arg Gly Leu Leu Met Leu Ser Val Ala			
1	5	10	15
Leu Gly Leu Thr Gln Gly Arg Leu Ala Lys Pro Ser Lys Leu Val Asn			
20	25	30	
Cys Thr Cys Glu Ser Pro His Cys Lys Arg Pro Phe Cys Gln Gly Ser			
35	40	45	
Trp Cys Thr Val Val Leu Val Arg Glu Gln Gly Arg His Pro Gln Val			
50	55	60	
Tyr Arg Gly Cys Gly Ser Leu Asn Gln Glu Leu Cys Leu Gly Arg Pro			
65	70	75	80
Thr Glu Phe Leu Asn His His Cys Cys Tyr Arg Ser Phe Cys Asn His			
85	90	95	
Asn Val Ser Leu Met Leu Glu Ala Thr Gln Thr Pro Ser Glu Glu Pro			
100	105	110	
Glu Val Asp Ala His Leu Pro Leu Ile Leu Gly Pro Val Leu Ala Leu			
115	120	125	
Pro Val Leu Val Ala Leu Gly Ala Leu Gly Leu Trp Arg Val Arg Arg			
130	135	140	
Arg Gln Glu Lys Gln Arg Asp Leu His Ser Asp Leu Gly Glu Ser Ser			
145	150	155	160
Leu Ile Leu Lys Ala Ser Glu Gln Ala Asp Ser Met Leu Gly Asp Phe			
165	170	175	
Leu Asp Ser Asp Cys Thr Thr Gly Ser Gly Leu Pro Phe Leu			
180	185	190	
Val Gln Arg Thr Val Ala Arg Gln Val Ala Leu Val Glu Cys Val Gly			
195	200	205	
Lys Gly Arg Tyr Gly Glu Val Trp Arg Gly Ser Trp His Gly Glu Ser			
210	215	220	
Val Ala Val Lys Ile Phe Ser Ser Arg Asp Glu Gln Ser Trp Phe Arg			
225	230	235	240
Glu Thr Glu Ile Tyr Asn Thr Val Leu Leu Arg His Asp Asn Ile Leu			
245	250	255	

Gly Phe Ile Ala Ser Asp Met Thr Ser Arg Asn Ser Ser Thr Gln Leu
260 265 270
Trp Leu Ile Thr His Tyr His Glu His Gly Ser Leu Tyr Asp Phe Leu
275 280 285
Gln Arg Gln Thr Leu Glu Pro Gln Leu Ala Leu Arg Leu Ala Val Ser
290 295 300
Pro Ala Cys Gly Leu Ala His Leu His Val Glu Ile Phe Gly Thr Gln
305 310 315 320
Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Arg Asn Val Leu
325 330 335
Val Lys Ser Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly Leu Ala Val
340 345 350
Met His Ser Gln Ser Asn Glu Tyr Leu Asp Ile Gly Asn Thr Pro Arg
355 360 365
Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu His Ile
370 375 380
Arg Thr Asp Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala Phe
385 390 395 400
Gly Leu Val Leu Trp Glu Ile Ala Arg Arg Thr Ile Ile Asn Gly Ile
405 410 415
Val Glu Asp Tyr Arg Pro Pro Phe Tyr Asp Met Val Pro Asn Asp Pro
420 425 430
Ser Phe Glu Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr Pro
435 440 445
Thr Ile Pro Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu Ala
450 455 460
Gln Met Met Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu Thr
465 470 475 480
Ala Leu Arg Ile Lys Lys Thr Leu Gln Lys Leu Ser His Asn Pro Glu
485 490 495
Lys Pro Lys Val Ile His
500

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2070 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mouse

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 217..1812

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

ATTCATGAGA	TGGAAGCATA	GGTCAAAGCT	GTTGGAGAA	ATTGGAACTA	CAGTTTATC	60
TAGCCACATC	TCTGAGAATT	CTGAAGAAAG	CAGCAGGTGA	AAGTCATTGC	CAAGTGATTT	120
TGTTCTGTAA	GGAAGCCTCC	CTCATTCACT	TACACCAGTG	AGACAGCAGG	ACCAGTCATT	180
CAAAGGGCCG	TGTACAGGAC	GCGTGGCAAT	CAGACA	ATG ACT CAG CTA TAC ACT		234
				Met Thr Gln Leu Tyr Thr		
				1	5	
TAC ATC AGA TTA CTG GGA GCC TGT CTG TTC ATC ATT TCT CAT GTT CAA						282
Tyr Ile Arg Leu Leu Gly Ala Cys Leu Phe Ile Ile Ser His Val Gln						
10	15	20				
GGG CAG AAT CTA GAT AGT ATG CTC CAT GGC ACT GGT ATG AAA TCA GAC						330
Gly Gln Asn Leu Asp Ser Met Leu His Gly Thr Gly Met Lys Ser Asp						
25	30	35				
TTG GAC CAG AAG CAA GAA AAT GGA GTG ACT TTA GCA CCA GAG GAT						378
Leu Asp Gln Lys Pro Glu Asn Gly Val Thr Leu Ala Pro Glu Asp						
40	45	50				
ACC TTG CCT TTC TTA AAG TGC TAT TGC TCA GGA CAC TGC CCA GAT GAT						426
Thr Leu Pro Phe Leu Lys Cys Tyr Cys Ser Gly His Cys Pro Asp Asp						
55	60	65			70	
GCT ATT AAT AAC ACA TGC ATA ACT AAT GGC CAT TGC TTT GCC ATT ATA						474
Ala Ile Asn Asn Thr Cys Ile Thr Asn Gly His Cys Phe Ala Ile Ile						
75	80	85				
GAA GAA GAT GAT CAG GGA GAA ACC ACA TTA ACT TCT GGG TGT ATG AAG						522
Glu Glu Asp Asp Gln Gly Glu Thr Thr Leu Thr Ser Gly Cys Met Lys						
90	95	100				
TAT GAA GGC TCT GAT TTT CAA TGC AAG GAT TCA CCG AAA GCC CAG CTA						570
Tyr Glu Gly Ser Asp Phe Gln Cys Lys Asp Ser Pro Lys Ala Gln Leu						
105	110	115				
CGC AGG ACA ATA GAA TGT TGT CGG ACC AAT TTG TGC AAC CAG TAT TTG						618
Arg Arg Thr Ile Glu Cys Cys Arg Thr Asn Leu Cys Asn Gln Tyr Leu						
120	125	130				
CAG CCT ACA CTG CCC CCT GTT ATA GGT CCG TTC TTT GAT GGC AGC						666
Gln Pro Thr Leu Pro Pro Val Val Ile Gly Pro Phe Phe Asp Gly Ser						
135	140	145			150	
ATC CGA TGG CTG GTT GTG CTC ATT TCC ATG GCT GTC TGT ATA GTT GCT						714
Ile Arg Trp Leu Val Val Leu Ile Ser Met Ala Val Cys Ile Val Ala						
155	160	165				

ATG ATC ATC TTC TCC AGC TGC TTT TGC TAT AAG CAT TAT TGT AAG AGT Met Ile Ile Phe Ser Ser Cys Phe Cys Tyr Lys His Tyr Cys Lys Ser 170 175 180	762
ATC TCA AGC AGG GGT CGT TAC AAC CGT GAT TTG GAA CAG GAT GAA GCA Ile Ser Ser Arg Gly Arg Tyr Asn Arg Asp Leu Glu Gln Asp Glu Ala 185 190 195	810
TTT ATT CCA GTA GGA GAA TCA TTG AAA GAC CTG ATT GAC CAG TCC CAA Phe Ile Pro Val Gly Glu Ser Leu Lys Asp Leu Ile Asp Gln Ser Gln 200 205 210	858
AGC TCT GGG AGT GGA TCT GGA TTG CCT TTA TTG GTT CAG CGA ACT ATT Ser Ser Gly Ser Gly Leu Pro Leu Leu Val Gln Arg Thr Ile 215 220 225 230	906
GCC AAA CAG ATT CAG ATG GTT CGG CAG GTT GGT AAA GGC CGC TAT GGA Ala Lys Gln Ile Gln Met Val Arg Gln Val Gly Lys Gly Arg Tyr Gly 235 240 245	954
GAA GTA TGG ATG GGT AAA TGG CGT GGT GAA AAA GTG GCT GTC AAA GTG Glu Val Trp Met Gly Lys Trp Arg Gly Glu Lys Val Ala Val Lys Val 250 255 260	1002
TTT TTT ACC ACT GAA GAA GCT AGC TGG TTT AGA GAA ACA GAA ATC TAC Phe Phe Thr Thr Glu Glu Ala Ser Trp Phe Arg Glu Thr Glu Ile Tyr 265 270 275	1050
CAG ACG GTG TTA ATG CGT CAT GAA AAT ATA CTT GGT TTT ATA GCT GCA Gln Thr Val Leu Met Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala 280 285 290	1098
GAC ATT AAA GGC ACT GGT TCC TGG ACT CAG CTG TAT TTG ATT ACT GAT Asp Ile Lys Gly Thr Gly Ser Trp Thr Gln Leu Tyr Leu Ile Thr Asp 295 300 305 310	1146
TAC CAT GAA AAT GGA TCT CTC TAT GAC TTC CTG AAA TGT GCC ACA CTA Tyr His Glu Asn Gly Ser Leu Tyr Asp Phe Leu Lys Cys Ala Thr Leu 315 320 325	1194
GAC ACC AGA GCC CTA CTC AAG TTA GCT TAT TCT GCT GCT TGT GGT CTG Asp Thr Arg Ala Leu Leu Lys Leu Ala Tyr Ser Ala Ala Cys Gly Leu 330 335 340	1242
TGC CAC CTC CAC ACA GAA ATT TAT GGT ACC CAA GGG AAG CCT GCA ATT Cys His Leu His Thr Glu Ile Tyr Gly Thr Gln Gly Lys Pro Ala Ile 345 350 355	1290
GCT CAT CGA GAC CTG AAG AGC AAA AAC ATC CTT ATT AAG AAA AAT GGA Ala His Arg Asp Leu Lys Ser Lys Asn Ile Leu Ile Lys Lys Asn Gly 360 365 370	1338

AGT TGC TGT ATT GCT GAC CTG GGC CTA GCT GTT AAA TTC AAC AGT GAT Ser Cys Cys Ile Ala Asp Leu Gly Leu Ala Val Lys Phe Asn Ser Asp 375 380 385 390	1386
ACA AAT GAA GTT GAC ATA CCC TTG AAT ACC AGG GTG GGC ACC AAG CGG Thr Asn Glu Val Asp Ile Pro Leu Asn Thr Arg Val Gly Thr Lys Arg 395 400 405	1434
TAC ATG GCT CCA GAA GTG CTG GAT GAA AGC CTG AAT AAA AAC CAT TTC Tyr Met Ala Pro Glu Val Leu Asp Glu Ser Leu Asn Lys Asn His Phe 410 415 420	1482
CAG CCC TAC ATC ATG GCT GAC ATC TAT AGC TTT GGT TTG ATC ATT TGG Gln Pro Tyr Ile Met Ala Asp Ile Tyr Ser Phe Gly Leu Ile Ile Trp 425 430 435	1530
GAA ATG GCT CGT CGT TGT ATT ACA GGA GGA ATC GTG GAG GAA TAT CAA Glu Met Ala Arg Arg Cys Ile Thr Gly Gly Ile Val Glu Glu Tyr Gln 440 445 450	1578
TTA CCA TAT TAC AAC ATG GTG CCC AGT GAC CCA TCC TAT GAG GAC ATG Leu Pro Tyr Tyr Asn Met Val Pro Ser Asp Pro Ser Tyr Glu Asp Met 455 460 465 470	1626
CGT GAG GTT GTG TGT GTG AAA CGC TTG CGG CCA ATC GTG TCT AAC CGC Arg Glu Val Val Cys Val Lys Arg Leu Arg Pro Ile Val Ser Asn Arg 475 480 485	1674
TGG AAC AGC GAT GAA TGT CTT CGA GCA GTT TTG AAG CTA ATG TCA GAA Trp Asn Ser Asp Glu Cys Leu Arg Ala Val Leu Lys Leu Met Ser Glu 490 495 500	1722
TGT TGG GCC CAT AAT CCA GCC TCC AGA CTC ACA GCT TTG AGA ATC AAG Cys Trp Ala His Asn Pro Ala Ser Arg Leu Thr Ala Leu Arg Ile Lys 505 510 515	1770
AAG ACA CTT GCA AAA ATG GTT GAA TCC CAG GAT GTA AAG ATT Lys Thr Leu Ala Lys Met Val Glu Ser Gln Asp Val Lys Ile 520 525 530	1812
TGACAATTAA ACAATTGGA GGGAGAATT AGACTGCAAG AACTCTTCA CCCAAGGAAT	1872
GGGTGGGATT AGCATGGAAT AGGATGTTGA CTTGGTTCC AGACTCCTTC CTCTACATCT	1932
TCACAGGCTG CTAACAGTAA ACCTTACCGT ACTCTACAGA ATACAAGATT GGAACCTGGAA	1992
ACTTCAAACA TGTCAATTCTT TATATATGAC AGCTTTGTTT TAATGTGGGG TTTTTTTGTT	2052
TGCTTTTTT GTTTTGTT	2070

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 532 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Met Thr Gln Leu Tyr Thr Tyr Ile Arg Leu Leu Gly Ala Cys Leu Phe
1 5 10 15
Ile Ile Ser His Val Gln Gly Gln Asn Leu Asp Ser Met Leu His Gly
20 25 30
Thr Gly Met Lys Ser Asp Leu Asp Gln Lys Lys Pro Glu Asn Gly Val
35 40 45
Thr Leu Ala Pro Glu Asp Thr Leu Pro Phe Leu Lys Cys Tyr Cys Ser
50 55 60
Gly His Cys Pro Asp Asp Ala Ile Asn Asn Thr Cys Ile Thr Asn Gly
65 70 75 80
His Cys Phe Ala Ile Ile Glu Glu Asp Asp Gln Gly Glu Thr Thr Leu
85 90 95
Thr Ser Gly Cys Met Lys Tyr Glu Gly Ser Asp Phe Gln Cys Lys Asp
100 105 110
Ser Pro Lys Ala Gln Leu Arg Arg Thr Ile Glu Cys Cys Arg Thr Asn
115 120 125
Leu Cys Asn Gln Tyr Leu Gln Pro Thr Leu Pro Pro Val Val Ile Gly
130 135 140
Pro Phe Phe Asp Gly Ser Ile Arg Trp Leu Val Val Leu Ile Ser Met
145 150 155 160
Ala Val Cys Ile Val Ala Met Ile Ile Phe Ser Ser Cys Phe Cys Tyr
165 170 175
Lys His Tyr Cys Lys Ser Ile Ser Ser Arg Gly Arg Tyr Asn Arg Asp
180 185 190
Leu Glu Gln Asp Glu Ala Phe Ile Pro Val Gly Glu Ser Leu Lys Asp
195 200 205
Leu Ile Asp Gln Ser Gln Ser Ser Gly Ser Gly Leu Pro Leu
210 215 220
Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met Val Arg Gln Val
225 230 235 240
Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys Trp Arg Gly Glu
245 250 255
Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu Ala Ser Trp Phe
260 265 270
Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg His Glu Asn Ile
275 280 285
Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly Ser Trp Thr Gln
290 295 300
Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser Leu Tyr Asp Phe
305 310 315 320
Leu Lys Cys Ala Thr Leu Asp Thr Arg Ala Leu Leu Lys Leu Ala Tyr
325 330 335
Ser Ala Ala Cys Gly Leu Cys His Leu His Thr Glu Ile Tyr Gly Thr
340 345 350
Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Lys Asn Ile
355 360 365

Leu Ile Lys Lys Asn Gly Ser Cys Cys Ile Ala Asp Leu Gly Leu Ala
 370 375 380
 Val Lys Phe Asn Ser Asp Thr Asn Glu Val Asp Ile Pro Leu Asn Thr
 385 390 395 400
 Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Ser
 405 410 415
 Leu Asn Lys Asn His Phe Gln Pro Tyr Ile Met Ala Asp Ile Tyr Ser
 420 425 430
 Phe Gly Leu Ile Ile Trp Glu Met Ala Arg Arg Cys Ile Thr Gly Gly
 435 440 445
 Ile Val Glu Glu Tyr Gln Leu Pro Tyr Tyr Asn Met Val Pro Ser Asp
 450 455 460
 Pro Ser Tyr Glu Asp Met Arg Glu Val Val Cys Val Lys Arg Leu Arg
 465 470 475 480
 Pro Ile Val Ser Asn Arg Trp Asn Ser Asp Glu Cys Leu Arg Ala Val
 485 490 495
 Leu Lys Leu Met Ser Glu Cys Trp Ala His Asn Pro Ala Ser Arg Leu
 500 505 510
 Thr Ala Leu Arg Ile Lys Lys Thr Leu Ala Lys Met Val Glu Ser Gln
 515 520 525
 Asp Val Lys Ile
 530

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2160 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mouse

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 10..1524

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CGCGGGTTAC ATG GCG GAG TCG GCC GGA GCC TCC TCC TTC TTC CCC CTT
 Met Ala Glu Ser Ala Gly Ala Ser Ser Phe Phe Pro Leu

1

5

10

GTT GTC CTC CTG CTC GCC GGC AGC GGC GGG TCC GGG CCC CGG GGG ATC Val Val Leu Leu Leu Ala Gly Ser Gly Gly Ser Gly Pro Arg Gly Ile 15 20 25	96
CAG GCT CTG CTG TGT GCG TGC ACC AGC TGC CTA CAG ACC AAC TAC ACC Gln Ala Leu Leu Cys Ala Cys Thr Ser Cys Leu Gln Thr Asn Tyr Thr 30 35 40 45	144
TGT GAG ACA GAT GGG GCT TGC ATG GTC TCC ATC TTT AAC CTG GAT GGC Cys Glu Thr Asp Gly Ala Cys Met Val Ser Ile Phe Asn Leu Asp Gly 50 55 60	192
GTG GAG CAC CAT GTA CGT ACC TGC ATC CCC AAG GTG GAG CTG GTT CCT Val Glu His His Val Arg Thr Cys Ile Pro Lys Val Glu Leu Val Pro 65 70 75	240
GCT GGA AAG CCC TTC TAC TGC CTG AGT TCA GAG GAT CTG CGC AAC ACA Ala Gly Lys Pro Phe Tyr Cys Leu Ser Ser Glu Asp Leu Arg Asn Thr 80 85 90	288
CAC TGC TGC TAT ATT GAC TTC TGC AAC AAG ATT GAC CTC AGG GTC CCC His Cys Cys Tyr Ile Asp Phe Cys Asn Lys Ile Asp Leu Arg Val Pro 95 100 105	336
AGC GGA CAC CTC AAG GAG CCT GCG CAC CCC TCC ATG TGG GGC CCT GTG Ser Gly His Leu Lys Glu Pro Ala His Pro Ser Met Trp Gly Pro Val 110 115 120 125	384
GAG CTG GTC GGC ATC ATC GCC GGC CCC GTC TTC CTC CTC TTC CTT ATC Glu Leu Val Gly Ile Ile Ala Gly Pro Val Phe Leu Leu Phe Leu Ile 130 135 140	432
ATT ATC ATC GTC TTC CTG GTC ATC AAC TAT CAC CAG CGT GTC TAC CAT Ile Ile Ile Val Phe Leu Val Ile Asn Tyr His Gln Arg Val Tyr His 145 150 155	480
AAC CGC CAG AGG TTG GAC ATG GAG GAC CCC TCT TGC GAG ATG TGT CTC Asn Arg Gln Arg Leu Asp Met Glu Asp Pro Ser Cys Glu Met Cys Leu 160 165 170	528
TCC AAA GAC AAG ACG CTC CAG GAT CTC GTC TAC GAC CTC TCC ACG TCA Ser Lys Asp Lys Thr Leu Gln Asp Leu Val Tyr Asp Leu Ser Thr Ser 175 180 185	576
GGG TCT GGC TCA GGG TTA CCC CTT TTT GTC CAG CGC ACA GTG GCC CGA Gly Ser Gly Ser Gly Leu Pro Leu Phe Val Gln Arg Thr Val Ala Arg 190 195 200 205	624
ACC ATT GTT TTA CAA GAG ATT ATC GGC AAG GGC CGG TTC GGG GAA GTA Thr Ile Val Leu Gln Glu Ile Ile Gly Lys Gly Arg Phe Gly Glu Val 210 215 220	672

TGG CGT GGT CGC TGG AGG GGT GGT GAC GTG GCT GTG AAA ATC TTC TCT Trp Arg Gly Arg Trp Arg Gly Gly Asp Val Ala Val Lys Ile Phe Ser 225 230 235	720
TCT CGT GAA GAA CGG TCT TGG TTC CGT GAA GCA GAG ATC TAC CAG ACC Ser Arg Glu Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr 240 245 250	768
GTC ATG CTG CGC CAT GAA AAC ATC CTT GGC TTT ATT GCT GCT GAC AAT Val Met Leu Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Asn 255 260 265	816
AAA GAT AAT GGC ACC TGG ACC CAG CTG TGG CTT GTC TCT GAC TAT CAC Lys Asp Asn Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Asp Tyr His 270 275 280 285	864
GAG CAT GGC TCA CTG TTT GAT TAT CTG AAC CGC TAC ACA GTG ACC ATT Glu His Gly Ser Leu Phe Asp Tyr Leu Asn Arg Tyr Thr Val Thr Ile 290 295 300	912
GAG GGA ATG ATT AAG CTA GCC TTG TCT GCA GCC AGT GGT TTG GCA CAC Glu Gly Met Ile Lys Leu Ala Leu Ser Ala Ala Ser Gly Leu Ala His 305 310 315	960
CTG CAT ATG GAG ATT GTG GGC ACT CAA GGG AAG CCG GGA ATT GCT CAT Leu His Met Glu Ile Val Gly Thr Gln Gly Lys Pro Gly Ile Ala His 320 325 330	1008
CGA GAC TTG AAG TCA AAG AAC ATC CTG GTG AAA AAA AAT GGC ATG TGT Arg Asp Leu Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Met Cys 335 340 345	1056
GCC ATT GCA GAC CTG GGC CTG GCT GTC CGT CAT GAT GCG GTC ACT GAC Ala Ile Ala Asp Leu Gly Leu Ala Val Arg His Asp Ala Val Thr Asp 350 355 360 365	1104
ACC ATA GAC ATT GCT CCA AAT CAG AGG GTG GGG ACC AAA CGA TAC ATG Thr Ile Asp Ile Ala Pro Asn Gln Arg Val Gly Thr Lys Arg Tyr Met 370 375 380	1152
GCT CCT GAA GTC CTT GAC GAG ACA ATC AAC ATG AAG CAC TTT GAC TCC Ala Pro Glu Val Leu Asp Glu Thr Ile Asn Met Lys His Phe Asp Ser 385 390 395	1200
TTC AAA TGT GCC GAC ATC TAT GCC CTC GGG CTT GTC TAC TGG GAG ATT Phe Lys Cys Ala Asp Ile Tyr Ala Leu Gly Leu Val Tyr Trp Glu Ile 400 405 410	1248
GCA CGA AGA TGC AAT TCT GGA GGA GTC CAT GAA GAC TAT CAA CTG CCG Ala Arg Arg Cys Asn Ser Gly Gly Val His Glu Asp Tyr Gln Leu Pro 415 420 425	1296

TAT TAC GAC TTA GTG CCC TCC GAC CCT TCC ATT GAG GAG ATG CGA AAG Tyr Tyr Asp Leu Val Pro Ser Asp Pro Ser Ile Glu Glu Met Arg Lys 430 435 440 445	1344
GTT GTA TGT GAC CAG AAG CTA CGG CCC AAT GTC CCC AAC TGG TGG CAG Val Val Cys Asp Gln Lys Leu Arg Pro Asn Val Pro Asn Trp Trp Gln 450 455 460	1392
AGT TAT GAG GCC TTG CGA GTG ATG GGA AAG ATG ATG CGG GAG TGC TGG Ser Tyr Glu Ala Leu Arg Val Met Gly Lys Met Met Arg Glu Cys Trp 465 470 475	1440
TAC GCC AAT GGT GCT GCC CGT CTG ACA GCT CTG CGC ATC AAG AAG ACT Tyr Ala Asn Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr 480 485 490	1488
CTG TCC CAG CTA AGC GTG CAG GAA GAT GTG AAG ATT TAAGCTGTTC Leu Ser Gln Leu Ser Val Gln Glu Asp Val Lys Ile 495 500 505	1534
CTCTGCCTAC ACAAAAGAACCC TGGGCAGTGA GGATGACTGC AGCCACCGTG CAAGCGTCGT GGAGGGCTAT CCTCTTGTCTT CTGCCCGGCC CTCTGGCAGA GCCCTGGCCT GCAAGAGGGA CAGAGCCTGG GAGACGCGCG CACTCCCGTT GGGTTTGAGA CAGACACTTT TTATATTTAC CTCCTGATGG CATGGAGACC TGAGCAAATC ATGTAGTCAC TCAATGCCAC AACTCAAAC GCTTCAGTGG GAAGTACAGA GACCCAGTGC ATTGCGTGTG CAGGAGCGTG AGGTGCTGGG CTCGCCAGGA GCGGCCCGCA TACCTTGTGG TCCACTGGC TGCAAGTTTT CCTCCAGGGA CCAGTCAACT GGCATCAAGA TATTGAGAGG AACCGGAAGT TTCTCCCTCC TTCCCGTAGC AGTCCTGAGC CACACCCTCC TTCTCATGGA CATCCGGAGG ACTGCCCTA GAGACACAAC CTGCTGCCTG TCTGTCCAGC CAAGTGCAGA TGTGCCGAGG TGTGTCCCAC ATTGTGCCTG GTCTGTGCCA CGCCCGTGTG TGTGTGTGTG TGTGTGAGTG AGTGTGTGTG TGTACACTTA ACCTGCTTGA GCTTCTGTGC ATGTGT	1594 1654 1714 1774 1834 1894 1954 2014 2074 2134 2160

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Met Ala Glu Ser Ala Gly Ala Ser Ser Phe Phe Pro Leu Val Val Leu
1 5 10 15
Leu Leu Ala Gly Ser Gly Gly Ser Gly Pro Arg Gly Ile Gln Ala Leu
20 25 30
Leu Cys Ala Cys Thr Ser Cys Leu Gln Thr Asn Tyr Thr Cys Glu Thr
35 40 45
Asp Gly Ala Cys Met Val Ser Ile Phe Asn Leu Asp Gly Val Glu His
50 55 60
His Val Arg Thr Cys Ile Pro Lys Val Glu Leu Val Pro Ala Gly Lys
65 70 75 80
Pro Phe Tyr Cys Leu Ser Ser Glu Asp Leu Arg Asn Thr His Cys Cys
85 90 95
Tyr Ile Asp Phe Cys Asn Lys Ile Asp Leu Arg Val Pro Ser Gly His
100 105 110
Leu Lys Glu Pro Ala His Pro Ser Met Trp Gly Pro Val Glu Leu Val
115 120 125
Gly Ile Ile Ala Gly Pro Val Phe Leu Leu Phe Leu Ile Ile Ile Ile
130 135 140
Val Phe Leu Val Ile Asn Tyr His Gln Arg Val Tyr His Asn Arg Gln
145 150 155 160
Arg Leu Asp Met Glu Asp Pro Ser Cys Glu Met Cys Leu Ser Lys Asp
165 170 175
Lys Thr Leu Gln Asp Leu Val Tyr Asp Leu Ser Thr Ser Gly Ser Gly
180 185 190
Ser Gly Leu Pro Leu Phe Val Gln Arg Thr Val Ala Arg Thr Ile Val
195 200 205
Leu Gln Glu Ile Ile Gly Lys Gly Arg Phe Gly Glu Val Trp Arg Gly
210 215 220
Arg Trp Arg Gly Gly Asp Val Ala Val Lys Ile Phe Ser Ser Arg Glu
225 230 235 240
Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr Val Met Leu
245 250 255
Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Asn Lys Asp Asn
260 265 270
Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Asp Tyr His Glu His Gly
275 280 285
Ser Leu Phe Asp Tyr Leu Asn Arg Tyr Thr Val Thr Ile Glu Gly Met
290 295 300
Ile Lys Leu Ala Leu Ser Ala Ala Ser Gly Leu Ala His Leu His Met
305 310 315 320
Glu Ile Val Gly Thr Gln Gly Lys Pro Gly Ile Ala His Arg Asp Leu
325 330 335
Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Met Cys Ala Ile Ala
340 345 350
Asp Leu Gly Leu Ala Val Arg His Asp Ala Val Thr Asp Thr Ile Asp
355 360 365
Ile Ala Pro Asn Gln Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu
370 375 380
Val Leu Asp Glu Thr Ile Asn Met Lys His Phe Asp Ser Phe Lys Cys
385 390 395 400
Ala Asp Ile Tyr Ala Leu Gly Leu Val Tyr Trp Glu Ile Ala Arg Arg
405 410 415
Cys Asn Ser Gly Gly Val His Glu Asp Tyr Gln Leu Pro Tyr Tyr Asp
420 425 430

Leu	Val	Pro	Ser	Asp	Pro	Ser	Ile	Glu	Glu	Met	Arg	Lys	Val	Val	Cys
435								440				445			
Asp	Gln	Lys	Leu	Arg	Pro	Asn	Val	Pro	Asn	Trp	Trp	Gln	Ser	Tyr	Glu
450								455				460			
Ala	Leu	Arg	Val	Met	Gly	Lys	Met	Met	Arg	Glu	Cys	Trp	Tyr	Ala	Asn
465								470			475				480
Gly	Ala	Ala	Arg	Leu	Thr	Ala	Leu	Arg	Ile	Lys	Lys	Thr	Leu	Ser	Gln
								485			490				495
Leu	Ser	Val	Gln	Glu	Asp	Val	Lys	Ile							
								500			505				

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1952 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mouse

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 187..1692

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

AAGCGGCGGC	AGAACGTTGCC	GGCGTGGTGC	TCGTAGTGAG	GGCGCGGAGG	ACCCGGGACC	60
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TGGGAAGCGG	CGGCAGGGTTA	ACTTCGGCTG	AATCACAACC	ATTTGGCGCT	GAGCTATGAC	120
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AAGAGAGCAA	ACAAAAAGTT	AAAGGAGCAA	CCCGGCCATA	AGTGAAGAGA	GAAGTTTATT	180
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GATAAC	ATG	CTC	TTA	CGA	AGC	TCT	GGA	AAA	TTA	AAT	GTG	GGC	ACC	AAG	228
Met	Leu	Leu	Arg	Ser	Ser	Gly	Lys	Leu	Asn	Val	Gly	Thr	Lys		
1						5					10				

AAG	GAG	GAT	GGA	GAG	AGT	ACA	GCC	CCC	ACC	CCT	CGG	CCC	AAG	ATC	CTA	276
Lys	Glu	Asp	Gly	Glu	Ser	Thr	Ala	Pro	Thr	Pro	Arg	Pro	Lys	Ile	Leu	
15						20				25			30			

CGT	TGT	AAA	TGC	CAC	CAC	TGT	CCG	GAA	GAC	TCA	GTC	AAC	AAT	ATC	324
Arg	Cys	Lys	Cys	His	His	Cys	Pro	Glu	Asp	Ser	Val	Asn	Asn	Ile	
							35			40			45		

TGC AGC ACA GAT GGG TAC TGC TTC ACG ATG ATA GAA GAA GAT GAC TCT Cys Ser Thr Asp Gly Tyr Cys Phe Thr Met Ile Glu Glu Asp Asp Ser 50 55 60	372
GGA ATG CCT GTT GTC ACC TCT GGA TGT CTA GGA CTA GAA GGG TCA GAT Gly Met Pro Val Val Thr Ser Gly Cys Leu Gly Leu Glu Gly Ser Asp 65 70 75	420
TTT CAA TGT CGT GAC ACT CCC ATT CCT CAT CAA AGA AGA TCA ATT GAA Phe Gln Cys Arg Asp Thr Pro Ile Pro His Gln Arg Arg Ser Ile Glu 80 85 90	468
TGC TGC ACA GAA AGG AAT GAG TGT AAT AAA GAC CTC CAC CCC ACT CTG Cys Cys Thr Glu Arg Asn Glu Cys Asn Lys Asp Leu His Pro Thr Leu 95 100 105 110	516
CCT CCT CTC AAG GAC AGA GAT TTT GTT GAT GGG CCC ATA CAC CAC AAG Pro Pro Leu Lys Asp Arg Asp Phe Val Asp Gly Pro Ile His His Lys 115 120 125	564
GCC TTG CTT ATC TCT GTG ACT GTC TGT AGT TTA CTC TTG GTC CTC ATT Ala Leu Leu Ile Ser Val Thr Val Asp Ser Leu Leu Leu Val Leu Ile 130 135 140	612
ATT TTA TTC TGT TAC TTC AGG TAT AAA AGA CAA GAA GCC CGA CCT CGG Ile Leu Phe Cys Tyr Phe Arg Tyr Lys Arg Gln Glu Ala Arg Pro Arg 145 150 155	660
TAC AGC ATT GGG CTG GAG CAG GAC GAG ACA TAC ATT CCT CCT GGA GAG Tyr Ser Ile Gly Leu Glu Gln Asp Glu Thr Tyr Ile Pro Pro Gly Glu 160 165 170	708
TCC CTG AGA GAC TTG ATC GAG CAG TCT CAG AGC TCG GGA AGT GGA TCA Ser Leu Arg Asp Leu Ile Glu Gln Ser Gln Ser Ser Gly Ser Gly Ser 175 180 185 190	756
GGC CTC CCT CTG CTG GTC CAA AGG ACA ATA GCT AAG CAA ATT CAG ATG Gly Leu Pro Leu Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met 195 200 205	804
GTG AAG CAG ATT GGA AAA GGC CGC TAT GGC GAG GTG TGG ATG GGA AAG Val Lys Gln Ile Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys 210 215 220	852
TGG CGT GGA GAA AAG GTG GCT GTG AAA GTG TTC TTC ACC ACG GAG GAA Trp Arg Gly Glu Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu 225 230 235	900
GCC AGC TGG TTC CGA GAG ACT GAG ATA TAT CAG ACG GTC CTG ATG CGG Ala Ser Trp Phe Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg 240 245 250	948

CAT GAG AAT ATT CTG GGG TTC ATT GCT GCA GAT ATC AAA GGG ACT GGG His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly 255 260 265 270	996
TCC TGG ACT CAG TTG TAC CTC ATC ACA GAC TAT CAT GAA AAC GGC TCC Ser Trp Thr Gln Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser 275 280 285	1044
CTT TAT GAC TAT CTG AAA TCC ACC ACC TTA GAC GCA AAG TCC ATG CTG Leu Tyr Asp Tyr Leu Lys Ser Thr Thr Leu Asp Ala Lys Ser Met Leu 290 295 300	1092
AAG CTA GCC TAC TCC TCT GTC AGC GGC CTA TGC CAT TTA CAC ACG GAA Lys Leu Ala Tyr Ser Ser Val Ser Gly Leu Cys His Leu His Thr Glu 305 310 315	1140
ATC TTT AGC ACT CAA GGC AAG CCA GCA ATC GCC CAT CGA GAC TTG AAA Ile Phe Ser Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys 320 325 330	1188
AGT AAA AAC ATC CTG GTG AAG AAA AAT GGA ACT TGC TGC ATA GCA GAC Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Thr Cys Cys Ile Ala Asp 335 340 345 350	1236
CTG GGC TTG GCT GTC AAG TTC ATT AGT GAC ACA AAT GAG GTT GAC ATC Leu Gly Leu Ala Val Lys Phe Ile Ser Asp Thr Asn Glu Val Asp Ile 355 360 365	1284
CCA CCC AAC ACC CGG GTT GGC ACC AAG CGC TAT ATG CCT CCA GAA GTG Pro Pro Asn Thr Arg Val Gly Thr Lys Arg Tyr Met Pro Pro Glu Val 370 375 380	1332
CTG GAC GAG AGC TTG AAT AGA AAC CAT TTC CAG TCC TAC ATT ATG GCT Leu Asp Glu Ser Leu Asn Arg Asn His Phe Gln Ser Tyr Ile Met Ala 385 390 395	1380
GAC ATG TAC AGC TTT GGA CTC ATC CTC TGG GAG ATT GCA AGG AGA TGT Asp Met Tyr Ser Phe Gly Leu Ile Leu Trp Glu Ile Ala Arg Arg Cys 400 405 410	1428
GTT TCT GGA GGT ATA GTG GAA GAA TAC CAG CTT CCC TAT CAC GAC CTG Val Ser Gly Gly Ile Val Glu Glu Tyr Gln Leu Pro Tyr His Asp Leu 415 420 425 430	1476
GTG CCC AGT GAC CCT TCT TAT GAG GAC ATG AGA GAA ATT GTG TGC ATG Val Pro Ser Asp Pro Ser Tyr Glu Asp Met Arg Glu Ile Val Cys Met 435 440 445	1524
AAG AAG TTA CGG CCT TCA TTC CCC AAT CGA TGG AGC AGT GAT GAG TGT Lys Lys Leu Arg Pro Ser Phe Pro Asn Arg Trp Ser Ser Asp Glu Cys 450 455 460	1572

CTC AGG CAG ATG GGG AAG CTT ATG ACA GAG TGC TGG GCG CAG AAT CCT Leu Arg Gln Met Gly Lys Leu Met Thr Glu Cys Trp Ala Gln Asn Pro 465 470 475	1620
GCC TCC AGG CTG ACG GCC CTG AGA GTT AAG AAA ACC CTT GCC AAA ATG Ala Ser Arg Leu Thr Ala Leu Arg Val Lys Lys Thr Leu Ala Lys Met 480 485 490	1668
TCA GAG TCC CAG GAC ATT AAA CTC TGACGTCAGA TACTTGTGGA CAGAGCAAGA Ser Glu Ser Gln Asp Ile Lys Leu 495 500	1722
ATTTCACAGA AGCATCGTTA GCCCAAGCCT TGAACGTTAG CCTACTGCC AGTGAGTTCA	1782
GACTTTCTG GAAGAGAGCA CGGTGGCAG ACACAGAGGA ACCCAGAAAC ACGGATTCAT	1842
CATGGCTTTC TGAGGGAGGAG AAACTGTTG GGTAACATTGT TCAAGATATG ATGCATGTTG	1902
CTTTCTAAGA AAGCCCTGTA TTTTGAATTA CCATTTTTT ATAAAAAAA	1952

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

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Met Leu Leu Arg Ser Ser Gly Lys Leu Asn Val Gly Thr Lys Lys Glu
1 5 10 15
Asp Gly Glu Ser Thr Ala Pro Thr Pro Arg Pro Lys Ile Leu Arg Cys
20 25 30
Lys Cys His His His Cys Pro Glu Asp Ser Val Asn Asn Ile Cys Ser
35 40 45
Thr Asp Gly Tyr Cys Phe Thr Met Ile Glu Glu Asp Asp Ser Gly Met
50 55 60
Pro Val Val Thr Ser Gly Cys Leu Gly Leu Glu Gly Ser Asp Phe Gln
65 70 75 80
Cys Arg Asp Thr Pro Ile Pro His Gln Arg Arg Ser Ile Glu Cys Cys
85 90 95
Thr Glu Arg Asn Glu Cys Asn Lys Asp Leu His Pro Thr Leu Pro Pro
100 105 110
Leu Lys Asp Arg Asp Phe Val Asp Gly Pro Ile His His Lys Ala Leu
115 120 125
Leu Ile Ser Val Thr Val Cys Ser Leu Leu Leu Val Leu Ile Ile Leu
130 135 140
Phe Cys Tyr Phe Arg Tyr Lys Arg Gln Glu Ala Arg Pro Arg Tyr Ser
145 150 155 160
Ile Gly Leu Glu Gln Asp Glu Thr Tyr Ile Pro Pro Gly Glu Ser Leu
165 170 175

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Arg Asp Leu Ile Glu Gln Ser Gln Ser Ser Gly Ser Gly Ser Gly Leu
 180 185 190
 Pro Leu Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met Val Lys
 195 200 205
 Gln Ile Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys Trp Arg
 210 215 220
 Gly Glu Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu Ala Ser
 225 230 235 240
 Trp Phe Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg His Glu
 245 250 255
 Asn Ile Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly Ser Trp
 260 265 270
 Thr Gln Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser Leu Tyr
 275 280 285
 Asp Tyr Leu Lys Ser Thr Thr Leu Asp Ala Lys Ser Met Leu Lys Leu
 290 295 300
 Ala Tyr Ser Ser Val Ser Gly Leu Cys His Leu His Thr Glu Ile Phe
 305 310 315 320
 Ser Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Lys
 325 330 335
 Asn Ile Leu Val Lys Lys Asn Gly Thr Cys Cys Ile Ala Asp Leu Gly
 340 345 350
 Leu Ala Val Lys Phe Ile Ser Asp Thr Asn Glu Val Asp Ile Pro Pro
 355 360 365
 Asn Thr Arg Val Gly Thr Lys Arg Tyr Met Pro Pro Glu Val Leu Asp
 370 375 380
 Glu Ser Leu Asn Arg Asn His Phe Gln Ser Tyr Ile Met Ala Asp Met
 385 390 395 400
 Tyr Ser Phe Gly Leu Ile Leu Trp Glu Ile Ala Arg Arg Cys Val Ser
 405 410 415
 Gly Gly Ile Val Glu Glu Tyr Gln Leu Pro Tyr His Asp Leu Val Pro
 420 425 430
 Ser Asp Pro Ser Tyr Glu Asp Met Arg Glu Ile Val Cys Met Lys Lys
 435 440 445
 Leu Arg Pro Ser Phe Pro Asn Arg Trp Ser Ser Asp Glu Cys Leu Arg
 450 455 460
 Gln Met Gly Lys Leu Met Thr Glu Cys Trp Ala Gln Asn Pro Ala Ser
 465 470 475 480
 Arg Leu Thr Ala Leu Arg Val Lys Lys Thr Leu Ala Lys Met Ser Glu
 485 490 495
 Ser Gln Asp Ile Lys Leu
 500

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

GCGGATCCTG TTGTGAAGGN AATATGTG

28

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

GCGATCCGTC GCAGTCAAAA TTTT

24

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GCGGATCCGC GATATATTAA AAGCAA

26

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

CGGAATTCTG GTGCCATATA

20

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

ATTCAAGGGC ACATCAACTT CATTGTGTC ACTGTTG

37

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

GCGGATCCAC CATGGCGGAG TCGGCC

26

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

AACACCGGGC CGGCGATGAT

20

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Gly Xaa Gly Xaa Xaa Gly
1 5

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

Asp Phe Lys Ser Arg Asn
1 5

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Asp Leu Lys Ser Lys Asn
1 5

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids

- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

Gly Thr Lys Arg Tyr Met
1 5

(2) INFORMATION FOR SEQ ID NO: 30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 182 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Leu Asp Thr Leu Val Gly Lys Gly Arg Phe Ala Glu Val Tyr Lys Ala
5 10 15
Lys Leu Lys Gln Asn Thr Ser Glu Gln Phe Glu Thr Val Ala Val Lys
20 25 30
Ile Phe Pro Tyr Asp His Tyr Ala Ser Trp Lys Asp Arg Lys Asp Ile
35 40 45
Phe Ser Asp Ile Asn Leu Lys His Glu Asn Ile Leu Gln Phe Leu Thr
50 55 60
Ala Glu Glu Arg Lys Thr Glu Leu Gly Lys Gln Tyr Trp Leu Ile Thr
65 70 75 80
Ala Phe His Ala Lys Gly Asn Leu Gln Glu Tyr Leu Thr Arg His Val
85 90 95
Ile Ser Trp Glu Asp Leu Arg Asn Val Gly Ser Ser Leu Ala Arg Gly
100 105 110
Leu Ser His Leu His Ser Asp His Thr Pro Cys Gly Arg Pro Lys Met
115 120 125
Pro Ile Val His Arg Asp Leu Lys Ser Ser Asn Ile Leu Val Lys Asn
130 135 140
Asp Leu Thr Cys Cys Leu Cys Asp Phe Gly Leu Ser Leu Arg Leu Gly
145 150 155 160
Pro Tyr Ser Ser Val Asp Asp Leu Ala Asn Ser Gly Gln Val Gly Thr
165 170 175
Ala Arg Tyr Met Ala Pro
180

(2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 176 amino acids
 - (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mouse

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

Leu Leu Glu Ile Lys Ala Arg Gly Arg Phe Gly Cys Val Trp Lys Ala
5 10 15
Gln Leu Met Asn Asp Phe Val Ala Val Lys Ile Phe Pro Leu Gln Asp
20 25 30
Lys Gln Ser Trp Gln Ser Glu Arg Glu Ile Phe Ser Thr Pro Gly Met
35 40 45
Lys His Glu Asn Leu Leu Gln Phe Ile Ala Ala Glu Lys Arg Gly Ser
50 55 60
Asn Leu Glu Val Glu Leu Trp Leu Ile Thr Ala Phe His Asp Lys Gly
65 70 75 80
Ser Leu Thr Asp Tyr Leu Lys Gly Asn Ile Ile Thr Trp Asn Glu Leu
85 90 95
Cys His Val Ala Glu Thr Met Ser Arg Gly Leu Ser Tyr Leu His Glu
100 105 110
Asp Val Pro Trp Cys Arg Gly Glu Gly His Lys Pro Ser Ile Ala His
115 120 125
Arg Asp Phe Lys Ser Lys Asn Val Leu Leu Lys Ser Asp Leu Thr Ala
130 135 140
Val Leu Ala Asp Phe Gly Leu Ala Val Arg Phe Glu Pro Gly Lys Pro
145 150 155 160
Pro Gly Asp Thr His Gly Gln Val Gly Thr Arg Arg Tyr Met Ala Pro
165 170 175

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mouse

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Leu Leu Glu Val Lys Ala Arg Gly Arg Phe Gly Cys Val Trp Lys Ala
5 10 15
Gln Leu Leu Asn Glu Tyr Val Ala Val Lys Ile Phe Pro Ile Gln Asp
20 25 30
Lys Gln Ser Trp Gln Asn Glu Tyr Glu Val Tyr Ser Leu Pro Gly Met
35 40 45
Lys His Glu Asn Ile Leu Gln Phe Ile Gly Ala Glu Lys Arg Gly Thr
50 55 60

Ser Val Asp Val Asp Leu Trp Leu Ile Thr Ala Phe His Glu Lys Gly
65 70 75 80
Ser Leu Ser Asp Phe Leu Lys Ala Asn Val Val Ser Trp Asn Glu Leu
85 90 95
Cys His Ile Ala Glu Thr Met Ala Arg Gly Leu Ala Tyr Leu His Glu
100 105 110
Asp Ile Pro Gly Leu Lys Asp Gly His Lys Pro Ala Ile Ser His Arg
115 120 125
Asp Ile Lys Ser Lys Asn Val Leu Leu Lys Asn Asn Leu Thr Ala Cys
130 135 140
Ile Ala Asp Phe Gly Leu Ala Leu Lys Phe Glu Ala Gly Lys Ser Ala
145 150 155 160
Gly Asp Thr His Gly Gln Val Gly Thr Arg Arg Tyr Met Ala Pro
165 170 175

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: C. elegans

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

Leu Thr Gly Arg Val Gly Ser Gly Arg Phe Gly Asn Val Ser Arg Gly
5 10 15
Asp Tyr Arg Gly Glu Ala Val Ala Val Lys Val Phe Asn Ala Leu Asp
20 25 30
Glu Pro Ala Phe His Lys Glu Thr Glu Ile Phe Glu Thr Arg Met Leu
35 40 45
Arg His Pro Asn Val Leu Arg Tyr Ile Gly Ser Asp Arg Val Asp Thr
50 55 60
Gly Phe Val Thr Glu Leu Trp Leu Val Thr Glu Tyr His Pro Ser Gly
65 70 75 80
Ser Leu His Asp Phe Leu Leu Glu Asn Thr Val Asn Ile Glu Thr Tyr
85 90 95
Tyr Asn Leu Met Arg Ser Thr Ala Ser Gly Leu Ala Phe Leu His Asn
100 105 110
Gln Ile Gly Gly Ser Lys Glu Ser Asn Lys Pro Ala Met Ala His Arg
115 120 125
Asp Ile Lys Ser Lys Asn Ile Met Val Lys Asn Asp Leu Thr Cys Ala
130 135 140
Ile Gly Asp Leu Gly Leu Ser Leu Ser Lys Pro Glu Asp Ala Ala Ser
145 150 155 160
Asp Ile Ile Ala Asn Glu Asn Tyr Lys Cys Gly Thr Val Arg Tyr Leu
165 170 175
Ala Pro

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: MOUSE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Met	Gly	Ala	Ala	Ala	Lys	Leu	Ala	Phe	Ala	Val	Phe	Leu	Ile	Ser	Cys
					5				10					15	
Ser	Ser	Gly	Ala	Ile	Leu	Gly	Arg	Ser	Glu	Thr	Gln	Glu	Cys	Leu	Phe
					20				25				30		
Phe	Asn	Ala	Asn	Trp	Glu	lys	Asp	Arg	Thr	Asn	Gln	Thr	Gly	Val	Glu
						35			40			45			
Pro	Cys	Tyr	Gly	Asp	Lys	Asp	Lys	Arg	Arg	His	Cys	Phe	Ala	Thr	Trp
						50			55		60				
Lys	Asn	Ile	Ser	Gly	Ser	Ile	Glu	Ile	Val	Lys	Gln	Gly	Cys	Trp	Leu
						65			70		75			80	
Asp	Asp	Ile	Asn	Cys	Tyr	Asp	Arg	Thr	Asp	Cys	Val	Glu	Lys	Lys	Asp
							85			90			95		
Ser	Pro	Glu	Val	Tyr	Phe	Cys	Cys	Cys	Glu	Gly	Asn	Met	Cys	Asn	Glu
						100			105				110		
Lys	Phe	Ser	Tyr	Phe	Pro	Glu	Met	Glu	Val	Thr	Gln	Pro	Thr	Ser	Asn
						115			120			125			
Pro	Val	Thr	Pro	Lys	Pro	Pro	Tyr	Tyr	Asn	Ile	Leu	Leu	Tyr	Ser	Leu
						130			135			140			
Val	Pro	Leu	Met	Leu	Ile	Ala	Gly	Ile	Val	Ile	Cys	Ala	Phe	Trp	Val
						145			150			155			160
Tyr	Arg	His	His	Lys	Met	Ala	Tyr	Pro	Pro	Val	Leu	Val	Pro	Thr	Gln
							165			170			175		
Asp	Pro	Gly	Pro	Pro	Pro	Pro	Ser	Pro	Leu	Leu	Gly	Leu	Lys	Pro	Leu
							180			185			190		
Gln	Leu	Leu	Glu	Val	Lys	Ala	Arg	Gly	Arg	Phe	Gly	Cys	Val	Trp	Lys
						195			200			205			
Ala	Gln	Leu	Leu	Asn	Glu	Tyr	Val	Ala	Val	Lys	Ile	Phe	Pro	Ile	Gln
						210			215			220			
Asp	Lys	Gln	Ser	Trp	Gln	Asn	Glu	Tyr	Glu	Val	Tyr	Ser	Leu	Pro	Gly
						225			230			235			240
Met	Lys	His	Glu	Asn	Ile	Leu	Gln	Phe	Ile	Gly	Ala	Glu	Lys	Arg	Gly
							245			250			255		
Thr	Ser	Val	Asp	Val	Asp	Leu	Trp	Leu	Ile	Thr	Ala	Phe	His	Glu	Lys
						260			265			270			
Gly	Ser	Leu	Ser	Asp	Phe	Leu	Lys	Ala	Asn	Val	Val	Ser	Trp	Asn	Glu
						275			280			285			
Leu	Cys	His	Ile	Ala	Glu	Thr	Met	Ala	Arg	Gly	Leu	Ala	Tyr	Leu	His
						290			295			300			
Glu	Asp	Ile	Pro	Gly	Leu	Lys	Asp	Gly	His	Lys	Pro	Ala	Ile	Ser	His
						305			310			315			320

Arg Asp Ile Lys Ser Lys Asn Val Leu Leu Lys Asn Asn Leu Thr Ala
 325 330 335
 Cys Ile Ala Asp Phe Gly Leu Ala Leu Lys Phe Glu Ala Gly Lys Ser
 340 345 350
 Ala Gly Asp Thr His Gly Gln Val Gly Thr Arg Arg Tyr Met Ala Pro
 355 360 365
 Glu Val Leu Glu Gly Ala Ile Asn Phe Gln Arg Asp Ala Phe Leu Arg
 370 375 380
 Ile Asp Met Tyr Ala Met Gly Leu Val Leu Trp Glu Leu Ala Ser Arg
 385 390 395 400
 Cys Thr Ala Ala Asp Gly Pro Val Asp Glu Tyr Met Leu Pro Phe Glu
 405 410 415
 Glu Glu Ile Gly Gln His Pro Ser Leu Glu Asp Met Gln Glu Val Val
 420 425 430
 Val His Lys Lys Arg Pro Val Leu Arg Asp Tyr Trp Gln Lys His
 435 440 445
 Ala Gly Met Ala Met Leu Cys Glu Thr Ile Glu Glu Cys Trp Asp His
 450 455 460
 Asp Ala Glu Ala Arg Leu Ser Ala Gly Cys Val Gly Glu Arg Ile Thr
 465 470 475 480
 Gln Met Gln Arg Leu Thr Asn Ile Ile Thr Thr Glu Asp Ile Val Thr
 485 490 495
 Val Val Thr Met Val Thr Asn Val Asp Phe Pro Pro Lys Glu Ser Ser
 500 505 510
 Leu

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: MOUSE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

Met Thr Ala Pro Trp Ala Ala Leu Ala Leu Trp Gly Ser Leu Cys
 5 10 15
 Ala Gly Ser Gly Arg Gly Glu Ala Glu Thr Arg Glu Cys Ile Tyr Tyr
 20 25 30
 Asn Ala Asn Trp Glu Leu Glu Arg Thr Asn Gln Ser Gly Leu Glu Arg
 35 40 45
 Cys Glu Gly Glu Gln Asp Lys Arg Leu His Cys Tyr Ala Ser Trp Arg
 50 55 60
 Asn Ser Ser Gly Thr Ile Glu Leu Val Lys Lys Gly Cys Trp Leu Asp
 65 70 75 80
 Asp Phe Asn Cys Tyr Asp Arg Gln Glu Cys Val Ala Thr Glu Glu Asn
 85 90 95
 Pro Gln Val Tyr Phe Cys Cys Cys Glu Gly Asn Phe Cys Asn Glu Arg
 100 105 110

Phe Thr His Leu Pro Glu Pro Gly Gly Pro Glu Val Thr Tyr Glu Pro
115 120 125
Pro Pro Thr Ala Pro Thr Leu Leu Thr Val Leu Ala Tyr Ser Leu Leu
130 135 140
Pro Ile Gly Gly Leu Ser Leu Ile Val Leu Leu Ala Phe Trp Met Tyr
145 150 155 160
Arg His Arg Lys Pro Pro Tyr Gly His Val Asp Ile His Glu Val Arg
165 170 175
Gln Cys Gln Arg Trp Ala Gly Arg Asp Gly Cys Ala Asp Ser Phe
180 185 190
Lys Pro Leu Pro Phe Gln Asp Pro Gly Pro Pro Pro Ser Pro Leu
195 200 205
Val Gly Leu Lys Pro Leu Gln Leu Leu Glu Ile Lys Ala Arg Gly Arg
210 215 220
Phe Gly Cys Val Trp Lys Ala Gln Leu Met Asn Asp Phe Val Ala Val
225 230 235 240
Lys Ile Phe Pro Leu Gln Asp Lys Gln Ser Trp Gln Ser Glu Arg Glu
245 250 255
Ile Phe Ser Thr Pro Gly Met Lys His Glu Asn Leu Leu Gln Phe Ile
260 265 270
Ala Ala Glu Lys Arg Gly Ser Asn Leu Glu Val Glu Leu Trp Leu Ile
275 280 285
Thr Ala Phe His Asp Lys Gly Ser Leu Thr Asp Tyr Leu Lys Gly Asn
290 295 300
Ile Ile Thr Trp Asn Glu Leu Cys His Val Ala Glu Thr Met Ser Arg
305 310 315 320
Gly Leu Ser Tyr Leu His Glu Asp Val Pro Trp Cys Arg Gly Glu Gly
325 330 335
His Lys Pro Ser Ile Ala His Arg Asp Phe Lys Ser Lys Asn Val Leu
340 345 350
Leu Lys Ser Asp Leu Thr Ala Val Leu Ala Asp Phe Gly Leu Ala Val
355 360 365
Arg Phe Glu Pro Gly Lys Pro Pro Gly Asp Thr His Gly Gln Val Gly
370 375 380
Thr Arg Arg Tyr Met Ala Pro Glu Val Leu Glu Gly Ala Ile Asn Phe
385 390 395 400
Gln Arg Asp Ala Phe Leu Arg Ile Asp Met Tyr Ala Met Gly Leu Val
405 410 415
Leu Trp Glu Leu Val Ser Arg Cys Lys Ala Ala Asp Gly Pro Val Asp
420 425 430
Glu Tyr Met Leu Pro Phe Glu Glu Ile Gly Gln His Pro Ser Leu
435 440 445
Glu Glu Leu Gln Glu Val Val His Lys Lys Met Arg Pro Thr Ile
450 455 460
Lys Asp His Trp Leu Lys His Pro Gly Leu Ala Gln Leu Cys Val Thr
465 470 475 480
Ile Glu Glu Cys Trp Asp His Asp Ala Glu Ala Arg Leu Ser Ala Gly
485 490 495
Cys Val Glu Glu Arg Val Ser Leu Ile Arg Arg Ser Val Asn Gly Thr
500 505 510
Thr Ser Asp Cys Leu Val Ser Leu Val Thr Ser Val Thr Asn Val Asp
515 520 525
Leu Leu Pro Lys Glu Ser Ser Ile
530 535

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 567 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

Tyr Trp Leu Ile Thr Ala Phe His Ala Lys Gly Asn Leu Gln Glu Tyr
 325 330 335
 Leu Thr Arg His Val Ile Ser Trp Glu Asp Leu Arg Lys Leu Gly Ser
 340 345 350
 Ser Leu Ala Arg Gly Ile Ala His Leu His Ser Asp His Thr Pro Cys
 355 360 365
 Gly Arg Pro Lys Met Pro Ile Val His Arg Asp Leu Lys Ser Ser Asn
 370 375 380
 Ile Leu Val Lys Asn Asp Leu Thr Cys Cys Leu Cys Asp Phe Gly Leu
 385 390 395 400
 Ser Leu Arg Leu Asp Pro Thr Leu Ser Val Asp Asp Leu Ala Asn Ser
 405 410 415
 Gly Gln Val Gly Thr Ala Arg Tyr Met Ala Pro Glu Val Leu Glu Ser
 420 425 430
 Arg Met Asn Leu Glu Asn Ala Glu Ser Phe Lys Gln Thr Asp Val Tyr
 435 440 445
 Ser Met Ala Leu Val Leu Trp Glu Met Thr Ser Arg Cys Asn Ala Val
 450 455 460
 Gly Glu Val Lys Asp Tyr Glu Pro Pro Phe Gly Ser Lys Val Arg Glu
 465 470 475 480
 His Pro Cys Val Glu Ser Met Lys Asp Asn Val Leu Arg Asp Arg Gly
 485 490 495
 Arg Pro Glu Ile Pro Ser Phe Trp Leu Asn His Gln Gly Ile Gln Met
 500 505 510
 Val Cys Glu Thr Leu Thr Glu Cys Trp Asp His Asp Pro Glu Ala Arg
 515 520 525
 Leu Thr Ala Gln Cys Val Ala Glu Arg Phe Ser Glu Leu Glu His Leu
 530 535 540
 Asp Arg Leu Ser Gly Arg Ser Cys Ser Glu Glu Lys Ile Pro Glu Asp
 545 550 555 560
 Gly Ser Leu Asn Thr Thr Lys
 565

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) ORGANISM: *C. elegans*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

Cys	His	Cys	Ser	Arg	Glu	Val	Gly	Cys	Asn	Ala	Arg	Thr	Thr	Gly	Trp
					5				10						15
Val	Pro	Gly	Ile	Glu	Phe	Leu	Asn	Glu	Thr	Asp	Arg	Ser	Phe	Tyr	Glu
								20		25				30	
Asn	Thr	Cys	Tyr	Thr	Asp	Gly	Ser	Cys	Tyr	Gln	Ser	Ala	Arg	Pro	Ser
								35		40				45	
Pro	Glu	Ile	Ser	His	Phe	Gly	Cys	Met	Asp	Glu	Lys	Ser	Val	Thr	Asp

50 55 60
Glu Thr Glu Phe His Asp Thr Ala Ala Lys Val Cys Thr Asn Asn Thr
65 70 75 80
Lys Asp Pro His Ala Thr Val Trp Ile Cys Cys Asp Lys Gly Asn Phe
85 90 100
Cys

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Asp Leu Lys Pro Glu Asn
5

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

Asp Leu Ala Ala Arg Asn
5

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Asp Ile Lys Ser Lys Asn
5

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

Asp Phe Lys Ser Lys Asn

5

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Asp Leu Lys Ser Ser Asn

5

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(D) OTHER INFORMATION: First Xaa is Thr or Ser;
fourth Xaa is Tyr or Phe; Each other Xaa
may be any amino acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

Gly Xaa Xaa Xaa Xaa Xaa

5

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(D) OTHER INFORMATION: First Xaa is any amino acid;
second Xaa is Ile or Val;
third Xaa is Lys or Arg;
fourth Xaa is Thr or Met.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

Xaa Pro Xaa Xaa Trp Xaa
5

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

Gly Thr Arg Arg Tyr Met
5

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Gly Thr Ala Arg Tyr Met
5

C
Cmt